GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 43 Seconds
(without alignments)
539.904 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 311

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	311	100.0	311	3	US-08-946-914-4	Sequence 4, Appli
2	311	100.0	311	4	US-09-656-450-4	Sequence 4, Appli
3	163	52.4	355	4	US-09-326-402C-18	Sequence 18, Appl
4	163	52.4	378	4	US-09-854-133-439	Sequence 439, App
5	148	47.6	168	4	US-09-401-064-199	Sequence 199, App
6	148	47.6	301	4	US-09-559-023-4	Sequence 4, Appli
7	87	28.0	323	4	US-09-326-402C-19	Sequence 19, Appl
8	69	22.2	145	2	US-08-788-584-1	Sequence 1, Appli
9	69	22.2	149	2	US-08-788-584-3	Sequence 3, Appli
10	22	7.1	322	4	US-09-559-023-2	Sequence 2, Appli
11	20	6.4	145	2	US-08-788-584-5	Sequence 5, Appli
12	20	6.4	145	3	US-08-946-914-12	Sequence 12, Appl
13	20	6.4	145	4	US-09-656-450-12	Sequence 12, Appl
14	20	6.4	145	4	US-09-557-170A-3	Sequence 3, Appli
15	12	3.9	262	3	US-08-946-914-14	Sequence 14, Appl
16	12	3.9	262	4	US-09-656-450-14	Sequence 14, Appl
17	10	3.2	275	4	US-09-557-170A-25	Sequence 25, Appl
18	10	3.2	296	4	US-09-557-170A-27	Sequence 27, Appl
19	10	3.2	324	3	US-08-946-914-11	Sequence 11, Appl
20	10	3.2	324	4	US-09-656-450-11	Sequence 11, Appl
21	10	3.2	336	3	US-09-131-648-1	Sequence 1, Appli
22	9	2.9	422	4	US-09-270-767-42572	Sequence 42572, A
23	8	2.6	43	4	US-08-875-553D-43	Sequence 43, Appl
24	8	2.6	45	4	US-08-875-553D-41	Sequence 41, Appl
25	8	2.6	45	4	US-08-875-553D-42	Sequence 42, Appl
26	8	2.6	46	4	US-08-875-553D-40	Sequence 40, Appl
27	8	2.6	143	4	US-09-877-790-1	Sequence 1, Appli
28	8	2.6	200	3	US-08-946-914-8	Sequence 8, Appli
29	8	2.6	200	4	US-09-656-450-8	Sequence 8, Appli
30	8	2.6	249	4	US-09-538-092-951	Sequence 951, App
31	8	2.6	250	1	US-08-562-311-2	Sequence 2, Appli
32	8	2.6	250	3	US-08-946-914-10	Sequence 10, Appl
33	8	2.6	250	4	US-09-656-450-10	Sequence 10, Appl
34	8	2.6	250	4	US-09-919-039-298	Sequence 298, App
35	8	2.6	250	4	US-09-877-790-2	Sequence 2, Appli
36	8	2.6	251	4	US-09-949-016-7560	Sequence 7560, Ap
37	8	2.6	264	1	US-08-562-311-4	Sequence 4, Appli
38	8	2.6	264	2	US-08-728-521-1	Sequence 1, Appli
39	8	2.6	264	3	US-09-212-146-1	Sequence 1, Appli
40	8	2.6	315	4	US-09-326-402C-17	Sequence 17, Appl
41	8	2.6	316	2	US-08-728-521-3	Sequence 3, Appli
42	8	2.6	316	2	US-08-647-960-2	Sequence 2, Appli
43	8	2.6	316	3	US-08-946-914-15	Sequence 15, Appl
44	8	2.6	316	3	US-08-946-914-17	Sequence 17, Appl
45	8	2.6	316	3	US-09-131-648-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-946-914-4
; Sequence 4, Application US/08946914
; Patent No. 6027916
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,914
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,093
; FILING DATE: 09-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-946-914-4

Query Match 100.0%; Score 311; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 9.2e-300;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

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Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180

Qy        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300

Qy        301 GGDIQLTHVQT 311
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Db        301 GGDIQLTHVQT 311


RESULT 2
US-09-656-450-4
; Sequence 4, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
;  FILE REFERENCE: 1488.0560003
;  CURRENT APPLICATION NUMBER: US/09/656,450
;  CURRENT FILING DATE:  2000-09-06
;  PRIOR APPLICATION NUMBER: US 09/263,689
;  PRIOR FILING DATE: 1999-03-05
;  PRIOR APPLICATION NUMBER: US 08/946,914
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: US 60/028,093
;  PRIOR FILING DATE: 1996-10-09
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-656-450-4

  Query Match            100.0%;  Score 311;  DB 4;  Length 311;
  Best Local Similarity  100.0%;  Pred. No. 9.2e-300;
  Matches  311;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
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Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180

Qy        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240
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Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
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Qy        301 GGDIQLTHVQT 311
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Db        301 GGDIQLTHVQT 311


RESULT 3
US-09-326-402C-18
; Sequence 18, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1
;  FILE REFERENCE: GEN-T112XC1
;  CURRENT APPLICATION NUMBER: US/09/326,402C
;  CURRENT FILING DATE:  1999-06-04
;  PRIOR APPLICATION NUMBER: 60/088,187
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/102,324
;  PRIOR FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(355)
;   OTHER INFORMATION: amino acid sequence of gal9-1
US-09-326-402C-18

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Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
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Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
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Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 4
US-09-854-133-439
; Sequence 439, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
;  APPLICANT: Lodes, Michael J.
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  THE THERAPY AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.475C10
;  CURRENT APPLICATION NUMBER: US/09/854,133
;  CURRENT FILING DATE:  2001-05-11
;  NUMBER OF SEQ ID NOS: 735
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 439
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-854-133-439
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  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        216 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 275

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 335

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Db        336 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 378


RESULT 5
US-09-401-064-199
; Sequence 199, Application US/09401064
; Patent No. 6623923
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT: Lodes, Michael J.
;  APPLICANT: Secrist, Heather
;  APPLICANT: Benson, Darin R.
;  APPLICANT: Meagher, Madeline Joy
;  APPLICANT: Stolk, John A.
;  APPLICANT: Wang, Tongtong
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
;  TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C2
;  CURRENT APPLICATION NUMBER: US/09/401,064
;  CURRENT FILING DATE: 1999-09-22
;  NUMBER OF SEQ ID NOS: 371
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 199
;   LENGTH: 168
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-401-064-199

  Query Match             47.6%;  Score 148;  DB 4;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-138;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          7 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 66

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 126

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQ 148
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Db        127 QYFHRVPFHRVDTISVNGSVQLSYISFQ 154


RESULT 6
US-09-559-023-4
; Sequence 4, Application US/09559023
; Patent No. 6551796
; GENERAL INFORMATION:
;  APPLICANT: Abramson, Ruth
;  APPLICANT:  Leal-Pinto, Edgar
;  APPLICANT:  Lipkowitz, Michael
;  TITLE OF INVENTION: NUCLEIC ACID ENCODING URATE TRANSPORTER
;  TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;  FILE REFERENCE: 070165.0574
;  CURRENT APPLICATION NUMBER: US/09/559,023
;  CURRENT FILING DATE:  2000-04-27
;  PRIOR APPLICATION NUMBER: US 09/221,898
;  PRIOR FILING DATE: 1998-12-28
;  PRIOR APPLICATION NUMBER: US 60/099,752
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/070,215
;  PRIOR FILING DATE: 1997-12-31
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 301
;   TYPE: PRT
;   ORGANISM: Human
US-09-559-023-4

  Query Match             47.6%;  Score 148;  DB 4;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-138;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQ 148
              ||||||||||||||||||||||||||||
Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQ 148


RESULT 7
US-09-326-402C-19
; Sequence 19, Application US/09326402C
; Patent No. 6759192
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1
;  FILE REFERENCE: GEN-T112XC1
;  CURRENT APPLICATION NUMBER: US/09/326,402C
;  CURRENT FILING DATE:  1999-06-04
;  PRIOR APPLICATION NUMBER: 60/088,187
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/102,324
;  PRIOR FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(323)
;   OTHER INFORMATION: amino acid sequence of gal
US-09-326-402C-19

  Query Match             28.0%;  Score 87;  DB 4;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-78;
  Matches   87;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 8
US-08-788-584-1
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; Sequence 1, Application US/08788584
; Patent No. 5837493
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Petithory, Joanne R.
;    TITLE OF INVENTION:  NOVEL HUMAN GALECTINS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/788,584
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0192 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-788-584-1

  Query Match             22.2%;  Score 69;  DB 2;  Length 145;
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  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        243 WGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGG 302
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Db         77 WGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGG 136

Qy        303 DIQLTHVQT 311
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Db        137 DIQLTHVQT 145


RESULT 9
US-08-788-584-3
; Sequence 3, Application US/08788584
; Patent No. 5837493
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Petithory, Joanne R.
;    TITLE OF INVENTION:  NOVEL HUMAN GALECTINS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/788,584
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0192 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  149 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-788-584-3

  Query Match             22.2%;  Score 69;  DB 2;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-60;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        243 WGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGG 302
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Db         81 WGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGG 140

Qy        303 DIQLTHVQT 311
              |||||||||
Db        141 DIQLTHVQT 149


RESULT 10
US-09-559-023-2
; Sequence 2, Application US/09559023
; Patent No. 6551796
; GENERAL INFORMATION:
;  APPLICANT: Abramson, Ruth
;  APPLICANT:  Leal-Pinto, Edgar
;  APPLICANT:  Lipkowitz, Michael
;  TITLE OF INVENTION: NUCLEIC ACID ENCODING URATE TRANSPORTER
;  TITLE OF INVENTION:  AND METHODS OF USE THEREOF
;  FILE REFERENCE: 070165.0574
;  CURRENT APPLICATION NUMBER: US/09/559,023
;  CURRENT FILING DATE:  2000-04-27
;  PRIOR APPLICATION NUMBER: US 09/221,898
;  PRIOR FILING DATE: 1998-12-28
;  PRIOR APPLICATION NUMBER: US 60/099,752
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/070,215
;  PRIOR FILING DATE: 1997-12-31
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 322
;   TYPE: PRT
;   ORGANISM: Rat
US-09-559-023-2

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Db          45 AVNFQTGFSGNDIAFHFNPRFE 66


RESULT 11
US-08-788-584-5
; Sequence 5, Application US/08788584
; Patent No. 5837493
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Hawkins, Phillip R.
;    APPLICANT:  Petithory, Joanne R.
;    TITLE OF INVENTION:  NOVEL HUMAN GALECTINS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/788,584
;      FILING DATE:  Filed Herewith
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0192 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  727176
US-08-788-584-5

  Query Match             6.4%;  Score 20;  DB 2;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 7e-12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 IAFHLNPRFDENAVVRNTQI 239
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Db         54 IAFHLNPRFDENAVVRNTQI 73


RESULT 12
US-08-946-914-12
; Sequence 12, Application US/08946914
; Patent No. 6027916
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Ruben, Steven M.
;    TITLE OF INVENTION:  Galectin 8, 9, 10 and 10SV
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein, & Fox P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/946,914
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,093
;      FILING DATE:  09-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0560001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  145 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-946-914-12

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  Best Local Similarity   100.0%;  Pred. No. 7e-12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 IAFHLNPRFDENAVVRNTQI 239
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Db         54 IAFHLNPRFDENAVVRNTQI 73


RESULT 13
US-09-656-450-12
; Sequence 12, Application US/09656450
; Patent No. 6468768
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
;  FILE REFERENCE: 1488.0560003
;  CURRENT APPLICATION NUMBER: US/09/656,450
;  CURRENT FILING DATE:  2000-09-06
;  PRIOR APPLICATION NUMBER: US 09/263,689
;  PRIOR FILING DATE: 1999-03-05
;  PRIOR APPLICATION NUMBER: US 08/946,914
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: US 60/028,093
;  PRIOR FILING DATE: 1996-10-09
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Rat
US-09-656-450-12

  Query Match             6.4%;  Score 20;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 7e-12;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 IAFHLNPRFDENAVVRNTQI 239
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Db         54 IAFHLNPRFDENAVVRNTQI 73


RESULT 14
US-09-557-170A-3
; Sequence 3, Application US/09557170A
; Patent No. 6605699
; GENERAL INFORMATION:
;  APPLICANT: Ni et al.
;  TITLE OF INVENTION: Galectin 11
;  FILE REFERENCE: PF354P2
;  CURRENT APPLICATION NUMBER: US/09/557,170A
;  CURRENT FILING DATE:  2000-04-21
;  PRIOR APPLICATION NUMBER: 09/109,864
;  PRIOR FILING DATE: 1998-06-06
;  PRIOR APPLICATION NUMBER: 09/010,146
;  PRIOR FILING DATE: 1998-01-21
;  PRIOR APPLICATION NUMBER: 60/034,205
;  PRIOR FILING DATE: 1997-01-21
;  PRIOR APPLICATION NUMBER: 60/034,204
;  PRIOR FILING DATE: 1997-01-21
;  PRIOR APPLICATION NUMBER: 60/169,932
;  PRIOR FILING DATE: 1999-12-10
;  PRIOR APPLICATION NUMBER: 60/130,390
;  PRIOR FILING DATE: 1999-04-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-557-170A-3

  Query Match             6.4%;  Score 20;  DB 4;  Length 145;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 IAFHLNPRFDENAVVRNTQI 239
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Db         54 IAFHLNPRFDENAVVRNTQI 73


RESULT 15
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; Sequence 14, Application US/08946914
; Patent No. 6027916
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Ruben, Steven M.
;    TITLE OF INVENTION:  Galectin 8, 9, 10 and 10SV
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein, & Fox P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/946,914
;      FILING DATE:  Herewith
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,093
;      FILING DATE:  09-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0560001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-946-914-14

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Db        164 GNDIAFHFNPRF 175


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Job time : 44 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:50:39 ; Search time 1430 Seconds
(without alignments)
84.020 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 311

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Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	311	100.0	311	14	US-10-235-674-4	Sequence 4, Appli
3	306	98.4	311	15	US-10-415-586-3	Sequence 3, Appli
4	163	52.4	323	9	US-09-728-479-2	Sequence 2, Appli
5	163	52.4	323	14	US-10-024-298A-141	Sequence 141, App
6	163	52.4	323	14	US-10-042-211A-141	Sequence 141, App
7	163	52.4	323	15	US-10-415-586-2	Sequence 2, Appli
8	163	52.4	323	15	US-10-617-217A-141	Sequence 141, App
9	163	52.4	323	16	US-10-024-298A-141	Sequence 141, App
10	163	52.4	355	14	US-10-376-133-18	Sequence 18, Appl
11	163	52.4	355	15	US-10-415-586-1	Sequence 1, Appli
12	163	52.4	355	15	US-10-633-035-2	Sequence 2, Appli
13	163	52.4	355	15	US-10-633-035-6	Sequence 6, Appli
14	163	52.4	355	16	US-10-856-888-18	Sequence 18, Appl
15	163	52.4	378	9	US-09-738-973-439	Sequence 439, App
16	163	52.4	378	9	US-09-854-133-439	Sequence 439, App
17	163	52.4	378	14	US-10-144-649A-439	Sequence 439, App
18	148	47.6	168	9	US-09-922-217-199	Sequence 199, App
19	148	47.6	168	9	US-09-833-263-199	Sequence 199, App
20	148	47.6	168	13	US-10-025-380-199	Sequence 199, App
21	103	33.1	123	15	US-10-424-599-143466	Sequence 143466,
22	87	28.0	322	15	US-10-633-035-7	Sequence 7, Appli
23	87	28.0	323	9	US-09-728-479-12	Sequence 12, Appl
24	87	28.0	323	16	US-10-856-888-19	Sequence 19, Appl
25	73	23.5	246	15	US-10-138-588-78	Sequence 78, Appl
26	69	22.2	145	9	US-09-894-526-1	Sequence 1, Appli
27	69	22.2	149	9	US-09-894-526-3	Sequence 3, Appli
28	68	21.9	353	15	US-10-633-035-8	Sequence 8, Appli
29	41	13.2	355	15	US-10-138-588-76	Sequence 76, Appl
30	38	12.2	97	9	US-09-925-301-1437	Sequence 1437, Ap
31	20	6.4	145	9	US-09-728-479-8	Sequence 8, Appli
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33	20	6.4	145	9	US-09-263-689-12	Sequence 12, Appl
34	20	6.4	145	14	US-10-235-674-12	Sequence 12, Appl
35	20	6.4	145	14	US-10-156-136-42	Sequence 42, Appl
36	20	6.4	145	15	US-10-455-366-3	Sequence 3, Appli
37	17	5.5	17	15	US-10-415-586-6	Sequence 6, Appli
38	17	5.5	29	15	US-10-415-586-5	Sequence 5, Appli
39	17	5.5	61	15	US-10-415-586-4	Sequence 4, Appli
40	13	4.2	322	9	US-09-728-479-11	Sequence 11, Appl
41	12	3.9	245	15	US-10-133-234A-6	Sequence 6, Appli
42	12	3.9	262	9	US-09-263-689-14	Sequence 14, Appl
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45	10	3.2	39	9	US-09-975-143-12	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-263-689-4
; Sequence 4, Application US/09263689
; Patent No. US20020150970A1
;  GENERAL INFORMATION:
;    APPLICANT:  Ni, Jian
;    APPLICANT:  Gentz, Reiner L.
;    APPLICANT:  Ruben, Steven M.
;    TITLE OF INVENTION:  Galectin 8, 9, 10 and 10SV
;    NUMBER OF SEQUENCES:  60
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein, & Fox P.L.L.C.
;      STREET:  1100 New York Ave., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,689
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/946,914
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1488.0560001/EKS/SGW
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  311 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-263-689-4

  Query Match            100.0%;  Score 311;  DB 9;  Length 311;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-283;
  Matches  311;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
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Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300

Qy        301 GGDIQLTHVQT 311
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Db        301 GGDIQLTHVQT 311


RESULT 2
US-10-235-674-4
; Sequence 4, Application US/10235674
; Publication No. US20030040081A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Gentz, Reiner L.
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Galectin 9 and 10SV Polynucleotides
;  FILE REFERENCE: 1488.0560004
;  CURRENT APPLICATION NUMBER: US/10/235,674
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 09/656,450
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: US 09/263,689
;  PRIOR FILING DATE: 1999-03-05
;  PRIOR APPLICATION NUMBER: US 08/946,914
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: US 60/028,093
;  PRIOR FILING DATE: 1996-10-09
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-235-674-4

  Query Match            100.0%;  Score 311;  DB 14;  Length 311;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-283;
  Matches  311;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180

Qy        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300

Qy        301 GGDIQLTHVQT 311
              |||||||||||
Db        301 GGDIQLTHVQT 311


RESULT 3
US-10-415-586-3
; Sequence 3, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
;  APPLICANT: HIRASHIMA, Mitsuomi
;  APPLICANT:  YAMAUCHI, Akira
;  APPLICANT:  KAGESHITA, Toshiro
;  APPLICANT:  NAKAMURA, Takanori
;  APPLICANT:  NISHI, No. US20040053346A1omu
;  TITLE OF INVENTION: Predicting agent for a metastasis
;  FILE REFERENCE: 2003-0572A/WMC/01332
;  CURRENT APPLICATION NUMBER: US/10/415,586
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: PCT/JP01/09561
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: JP 2000-335077
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 311
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-415-586-3

  Query Match            98.4%;  Score 306;  DB 15;  Length 311;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-279;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 SQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPR 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 SQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPR 65

Qy         66 FEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHR 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 FEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHR 125

Qy        126 VPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFIT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 VPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFIT 185

Qy        186 TILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245

Qy        246 EERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQ 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 EERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQ 305
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Qy        306 LTHVQT 311
              ||||||
Db        306 LTHVQT 311


RESULT 4
US-09-728-479-2
; Sequence 2, Application US/09728479
; Patent No. US20020034726A1
; GENERAL INFORMATION:
;  APPLICANT: KANEGASAKI, SHIRO
;  APPLICANT:  MATSUMOTO, RYOJI
;  APPLICANT:  HIRASHIMA, MITSUOMI
;  TITLE OF INVENTION: EOSINOPHIL CHEMOTACTIC FACTOR
;  FILE REFERENCE: 3914-2
;  CURRENT APPLICATION NUMBER: US/09/728,479
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/02952
;  PRIOR FILING DATE: 1999-06-02
;  PRIOR APPLICATION NUMBER: JP 10/170698
;  PRIOR FILING DATE: 1998-06-02
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-728-479-2

  Query Match             52.4%;  Score 163;  DB 9;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 5
US-10-024-298A-141
; Sequence 141, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
;  APPLICANT:  Akio MATSUDA
;  APPLICANT:  Goichi HONDA
;  APPLICANT:  Shuji MURAMATSU
;  APPLICANT:  Yukiko NAGANO
;  TITLE OF INVENTION: NF-K B Activating Gene
;  FILE REFERENCE: 1254-0191P
;  CURRENT APPLICATION NUMBER: US/10/024,298A
;  CURRENT FILING DATE:  2003-04-08
;  PRIOR APPLICATION NUMBER: 60/314,385
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/278,641
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: 60/258,315
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP254018/2001
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: JP0088912/2001
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: JP402288/2000
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-024-298A-141

  Query Match             52.4%;  Score 163;  DB 14;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 6
US-10-042-211A-141
; Sequence 141, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
;  APPLICANT: MATSUDA, Akio et al.
;  TITLE OF INVENTION: NFKB Activating Gene
;  FILE REFERENCE: 1254-0192P
;  CURRENT APPLICATION NUMBER: US/10/042,211A
;  CURRENT FILING DATE:  2002-01-11
;  PRIOR APPLICATION NUMBER: JP 2000-402288
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP 2001-088912
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-254018
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/258,315
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: US 60/278,640
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 60/314,385
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-042-211A-141

  Query Match             52.4%;  Score 163;  DB 14;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 7
US-10-415-586-2
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; Sequence 2, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
;  APPLICANT: HIRASHIMA, Mitsuomi
;  APPLICANT:  YAMAUCHI, Akira
;  APPLICANT:  KAGESHITA, Toshiro
;  APPLICANT:  NAKAMURA, Takanori
;  APPLICANT:  NISHI, No. US20040053346A1omu
;  TITLE OF INVENTION: Predicting agent for a metastasis
;  FILE REFERENCE: 2003-0572A/WMC/01332
;  CURRENT APPLICATION NUMBER: US/10/415,586
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: PCT/JP01/09561
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: JP 2000-335077
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-415-586-2

  Query Match             52.4%;  Score 163;  DB 15;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 8
US-10-617-217A-141
; Sequence 141, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
;  APPLICANT: MATSUDA, Akio et al.
;  TITLE OF INVENTION: NF-kB ACTIVATING GENE
;  FILE REFERENCE: 1254-0229P
;  CURRENT APPLICATION NUMBER: US/10/617,217A
;  CURRENT FILING DATE:  2003-07-11
;  PRIOR APPLICATION NUMBER: JP 2000-402288
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP 2001-088912
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: JP 2001-254018
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/258,315
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: US 60/278,640
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 60/314,385
;  PRIOR FILING DATE: 2001-08-24
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-617-217A-141

  Query Match             52.4%;  Score 163;  DB 15;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 9
US-10-024-298A-141
; Sequence 141, Application US/10024298A
; Publication No. US20040214167A9
; GENERAL INFORMATION:
;  APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
;  APPLICANT:  Akio MATSUDA
;  APPLICANT:  Goichi HONDA
;  APPLICANT:  Shuji MURAMATSU
;  APPLICANT:  Yukiko NAGANO
;  TITLE OF INVENTION: NF-K B Activating Gene
;  FILE REFERENCE: 1254-0191P
;  CURRENT APPLICATION NUMBER: US/10/024,298A
;  CURRENT FILING DATE:  2003-04-08
;  PRIOR APPLICATION NUMBER: 60/314,385
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/278,641
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: 60/258,315
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: JP254018/2001
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: JP0088912/2001
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: JP402288/2000
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
;   LENGTH: 323
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-024-298A-141

  Query Match             52.4%;  Score 163;  DB 16;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323


RESULT 10
US-10-376-133-18
; Sequence 18, Application US/10376133
; Publication No. US20030165965A1
; GENERAL INFORMATION:
;  APPLICANT: EXELIXIS, INC.
;  TITLE OF INVENTION: LGALS AS MODIFIERS OF THE CHK PATHWAY AND METHODS OF USE
```

```
;  FILE REFERENCE: EX03-014C
;  CURRENT APPLICATION NUMBER: US/10/376,133
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,757
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-376-133-18

  Query Match             52.4%;  Score 163;  DB 14;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 11
US-10-415-586-1
; Sequence 1, Application US/10415586
; Publication No. US20040053346A1
; GENERAL INFORMATION:
;  APPLICANT: HIRASHIMA, Mitsuomi
;  APPLICANT:  YAMAUCHI, Akira
;  APPLICANT:  KAGESHITA, Toshiro
;  APPLICANT:  NAKAMURA, Takanori
;  APPLICANT:  NISHI, No. US20040053346A1omu
;  TITLE OF INVENTION: Predicting agent for a metastasis
;  FILE REFERENCE: 2003-0572A/WMC/01332
;  CURRENT APPLICATION NUMBER: US/10/415,586
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: PCT/JP01/09561
;  PRIOR FILING DATE: 2001-10-31
;  PRIOR APPLICATION NUMBER: JP 2000-335077
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-415-586-1

  Query Match             52.4%;  Score 163;  DB 15;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
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Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 12
US-10-633-035-2
; Sequence 2, Application US/10633035
; Publication No. US20040068104A1
; GENERAL INFORMATION:
;  APPLICANT: Seisi Kato
;  APPLICANT:  Yamaguchi Kimura
;  APPLICANT:  Shingo Sekine
;  APPLICANT:  Kouju Kamata
;  TITLE OF INVENTION: HUMAN GALECTIC-9-LIKE PROTEINS AND cDNA ENCODING THESE
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: GIN-6707CPUS
;  CURRENT APPLICATION NUMBER: US/10/633,035
;  CURRENT FILING DATE:  2003-08-04
;  PRIOR APPLICATION NUMBER: US/09/485,951
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 9-226468
;  PRIOR FILING DATE: 1997-08-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/03670
;  PRIOR FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-633-035-2

  Query Match             52.4%;  Score 163;  DB 15;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
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Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
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Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 13
US-10-633-035-6
; Sequence 6, Application US/10633035
; Publication No. US20040068104A1
; GENERAL INFORMATION:
;  APPLICANT: Seisi Kato
;  APPLICANT:  Yamaguchi Kimura
;  APPLICANT:  Shingo Sekine
;  APPLICANT:  Kouju Kamata
;  TITLE OF INVENTION: HUMAN GALECTIC-9-LIKE PROTEINS AND cDNA ENCODING THESE
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: GIN-6707CPUS
;  CURRENT APPLICATION NUMBER: US/10/633,035
;  CURRENT FILING DATE:  2003-08-04
;  PRIOR APPLICATION NUMBER: US/09/485,951
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 9-226468
;  PRIOR FILING DATE: 1997-08-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/03670
;  PRIOR FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-633-035-6
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  Query Match            52.4%;  Score 163;  DB 15;  Length 355;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
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Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 14
US-10-856-888-18
; Sequence 18, Application US/10856888
; Publication No. US20040235037A1
; GENERAL INFORMATION:
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Polymorphic Markers of Prostate Carcinoma Tumor Antigen-1 (PCTA-1
;  FILE REFERENCE: GEN-T112XC1
;  CURRENT APPLICATION NUMBER: US/10/856,888
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US/09/326,402
;  PRIOR FILING DATE: 1999-06-04
;  PRIOR APPLICATION NUMBER: 60/088,187
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/102,324
;  PRIOR FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(355)
;   OTHER INFORMATION: amino acid sequence of gal9-1
US-10-856-888-18

  Query Match            52.4%;  Score 163;  DB 16;  Length 355;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 15
US-09-738-973-439
; Sequence 439, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Fling, Steven P.
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Algate, Paul A.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Indirias, Carol Yoseph
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Elliot, Mark
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Kalos, Michael D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  THE THERAPY AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.475C9
;  CURRENT APPLICATION NUMBER: US/09/738,973
;  CURRENT FILING DATE:  2000-12-14
;  NUMBER OF SEQ ID NOS:  587
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 439
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-738-973-439

  Query Match            52.4%;  Score 163;  DB 9;  Length 378;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-144;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 275

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
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Db        276 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 335

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
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Search completed: July 13, 2005, 08:34:36
Job time : 1432 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 311

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	311	100.0	311	2	Q8WYQ7	Q8wyq7 homo sapien
2	163	52.4	355	1	LEG9_HUMAN	O00182 homo sapien
3	41	13.2	356	2	Q6DKI2	Q6dki2 homo sapien
4	22	7.1	322	2	Q6P7Q6	Q6p7q6 rattus norv
5	22	7.1	354	1	LEG9_RAT	P97840 rattus norv
6	20	6.4	144	1	LEG5_RAT	P47967 rattus norv
7	17	5.5	323	2	Q6QZP2	Q6qzp2 canis famil
8	16	5.1	317	2	Q9XSM8	Q9xsm8 sus scrofa
9	16	5.1	349	2	Q9XSM9	Q9xsm9 sus scrofa
10	13	4.2	322	2	Q99L83	Q99l83 mus musculu
11	13	4.2	353	1	LEG9_MOUSE	O08573 mus musculu
12	12	3.9	244	1	LEG3_CRILO	P47953 cricetulus
13	12	3.9	261	1	LEG3_RAT	P08699 rattus norv
14	11	3.5	332	2	Q8UW97	Q8uw97 xenopus lae
15	11	3.5	353	2	Q6PGR5	Q6pgr5 xenopus lae
16	10	3.2	262	2	Q90713	Q90713 gallus gall
17	10	3.2	296	2	Q9NZ03	Q9nz03 homo sapien
18	10	3.2	308	2	Q7ZTB8	Q7ztb8 xenopus lae
19	10	3.2	324	1	LEG4_RAT	P38552 rattus norv
20	10	3.2	328	2	Q86GY9	Q86gy9 rhipicephal
21	10	3.2	328	2	Q9TUB8	Q9tub8 oryctolagus
22	10	3.2	332	2	Q8QGD9	Q8qgd9 gallus gall
23	10	3.2	336	1	LEGC_HUMAN	Q96dt0 homo sapien
24	9	2.9	162	2	Q8WN59	Q8wn59 ovis aries
25	9	2.9	265	2	Q941Y9	Q941y9 oryza sativ
26	9	2.9	503	2	Q9VPI6	Q9vpi6 drosophila
27	8	2.6	48	2	Q9QWA2	Q9qwa2 rattus sp.
28	8	2.6	119	2	Q85FV3	Q85fv3 cyanidiosch
29	8	2.6	121	2	Q86TY5	Q86ty5 homo sapien
30	8	2.6	122	2	Q8KAI2	Q8kai2 chlorobium
31	8	2.6	139	2	Q61357	Q61357 mus musculu
32	8	2.6	139	2	Q6DGJ1	Q6dgj1 brachydanio
33	8	2.6	180	2	Q7T120	Q7t120 brachydanio
34	8	2.6	241	1	LEG3_RABIT	P47845 oryctolagus
35	8	2.6	249	1	LEG3_HUMAN	P17931 homo sapien
36	8	2.6	250	2	Q6FGL0	Q6fgl0 homo sapien
37	8	2.6	250	2	Q6IBA7	Q6iba7 homo sapien
38	8	2.6	250	2	Q6NVH9	Q6nvh9 homo sapien
39	8	2.6	263	1	LEG3_MOUSE	P16110 mus musculu
40	8	2.6	264	2	Q8C253	Q8c253 mus musculu
41	8	2.6	295	1	LEG3_CANFA	P38486 canis famil
42	8	2.6	300	2	Q96QS7	Q96qs7 homo sapien
43	8	2.6	301	1	LEG6_MOUSE	O54891 mus musculu
44	8	2.6	310	2	Q6PBV2	Q6pbv2 brachydanio
45	8	2.6	310	2	Q7T118	Q7t118 brachydanio

ALIGNMENTS

RESULT 1
Q8WYQ7
ID Q8WYQ7 PRELIMINARY; PRT; 311 AA.
AC Q8WYQ7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Galectin-9.
GN Name=LGALS9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Akiyama S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR EMBL; AB040130; BAB83623.1; -.
DR EMBL; AB040129; BAB83623.1; JOINED.
DR HSSP; P17931; 1A3K.
DR GO; GO:0005529; F:sugar binding; IEA.
DR Pfam; PF00337; Gal-bind_lectin; 2.
DR SMART; SM00276; GLECT; 2.
DR PROSITE; PS00309; GALAPTIN; 2.
KW Galectin; Lectin.
SQ SEQUENCE 311 AA; 34690 MW; 3D00232FE39D776C CRC64;

Query Match 100.0%; Score 311; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60
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Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
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Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
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Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180

Qy        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240
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Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
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Db        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300

Qy        301 GGDIQLTHVQT 311
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Db        301 GGDIQLTHVQT 311


RESULT 2
LEG9_HUMAN
ID   LEG9_HUMAN     STANDARD;      PRT;   355 AA.
AC   O00182; O14532; O75028; Q9NQ58;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-9 (HOM-HD-21) (Ecalectin).
GN   Name=LGALS9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   TISSUE=Spleen;
RX   MEDLINE=97197815; PubMed=9045665; DOI=10.1074/jbc.272.10.6416;
RA   Tuereci O., Schmitt H., Fadle N., Pfreundschuh M., Sahin U.;
RT   "Molecular definition of a novel human galectin which is immunogenic
RT   in patients with Hodgkin's disease.";
RL   J. Biol. Chem. 272:6416-6422(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RC   TISSUE=Gastric carcinoma;
RA   Kato S.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RX   MEDLINE=98307937; PubMed=9642261; DOI=10.1074/jbc.273.27.16976;
RA   Matsumoto R., Matsumoto H., Seki M., Hata M., Asano Y., Kanegasaki S.,
RA   Stevens R.L., Hirashima M.;
RT   "Human ecalectin, a variant of human galectin-9, is a novel eosinophil
RT   chemoattractant produced by T lymphocytes.";
RL   J. Biol. Chem. 273:16976-16984(1998).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RA   Akiyama S.;
RT   "Homo sapiens galectin-9 (LGALS9) / ecalectin gene, exon 2 through
RT   11.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RA   Graessler J., Spitzenberger F., Schroeder H.E.;
RT   "Genomic organization of the human galectin-9 gene.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Binds galactosides. May play a role in thymocyte-
CC       epithelial interactions relevant to the biology of the thymus. The
CC       short isoform acts as an eosinophil chemoattractant.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=Long;
CC         IsoId=O00182-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=O00182-2; Sequence=VSP_003096;
CC   -!- TISSUE SPECIFICITY: Peripheral blood leukocytes and lymphatic
CC       tissues. Overexpressed in Hodgkin's disease tissue.
CC   -!- DOMAIN: Contains two homologous but distinct carbohydrate-binding
CC       domains.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z49107; CAA88922.1; -.
DR   EMBL; AB006782; BAA22166.1; -.
DR   EMBL; AB005894; BAA31542.1; -.
DR   EMBL; AB040130; BAB83625.1; -.
DR   EMBL; AB040129; BAB83625.1; JOINED.
DR   EMBL; AB040130; BAB83624.1; -.
DR   EMBL; AB040129; BAB83624.1; JOINED.
DR   EMBL; AJ288083; CAB93851.1; -.
DR   EMBL; AJ288084; CAB93851.1; JOINED.
DR   EMBL; AJ288085; CAB93851.1; JOINED.
DR   EMBL; AJ288086; CAB93851.1; JOINED.
DR   EMBL; AJ288087; CAB93851.1; JOINED.
DR   EMBL; AJ288088; CAB93851.1; JOINED.
DR   EMBL; AJ288089; CAB93851.1; JOINED.
DR   EMBL; AJ288090; CAB93851.1; JOINED.
DR   HSSP; P17931; 1A3K.
DR   Genew; HGNC:6570; LGALS9.
DR   MIM; 601879; -.
DR   GO; GO:0005534; F:galactose binding; TAS.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Alternative splicing; Galectin; Lectin; Repeat.
FT   DOMAIN       1    148       Galaptin 1.
FT   DOMAIN     149    206       Linker.
FT   DOMAIN     207    355       Galaptin 2.
FT   SITE        82     88       Beta-galactoside binding 1 (By
FT                               similarity).
FT   SITE       287    293       Beta-galactoside binding 2 (By
FT                               similarity).
FT   VARSPLIC   149    180       Missing (in isoform Short).
FT                               /FTId=VSP_003096.
FT   CONFLICT     5      5       G -> S (in Ref. 3).
FT   CONFLICT    48     48       N -> D (in Ref. 5).
FT   CONFLICT    79     81       NGS -> KGR (in Ref. 5).
FT   CONFLICT    88     88       K -> R (in Ref. 1).
FT   CONFLICT    89     89       T -> M (in Ref. 5).
FT   CONFLICT   135    135       S -> F (in Ref. 1).
FT   CONFLICT   270    270       P -> L (in Ref. 1).
FT   CONFLICT   313    313       E -> G (in Ref. 1).
FT   CONFLICT   326    326       L -> V (in Ref. 5).
FT   CONFLICT   341    341       R -> K (in Ref. 5).
SQ   SEQUENCE   355 AA;  39518 MW;  4748C22FCAFA536A CRC64;

  Query Match             52.4%;  Score 163;  DB 1;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-162;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 3
Q6DKI2
ID   Q6DKI2      PRELIMINARY;      PRT;   356 AA.
AC   Q6DKI2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

```
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; BC073889; AAH73889.1; -.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Galectin; Hypothetical protein; Lectin.
SQ   SEQUENCE   356 AA;  39633 MW;  933AD3A82B84784C CRC64;

  Query Match             13.2%;  Score 41;  DB 2;  Length 356;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-34;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQH 281
              |||||||||||||||||||||||||||||||||||||||||||
Db        286 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQH 326


RESULT 4
Q6P7Q6
ID   Q6P7Q6      PRELIMINARY;      PRT;   322 AA.
AC   Q6P7Q6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Lectin, galactose binding, soluble 9.
GN   Name=Lgals9;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary gland;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; BC061566; AAH61566.1; -.
DR   HSSP; P17931; 1A3K.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Galectin; Lectin.
SQ   SEQUENCE   322 AA;  36341 MW;  CDD414A6FD1BA9DD CRC64;

  Query Match             7.1%;  Score 22;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-14;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 AVNFQTGFSGNDIAFHFNPRFE 67
              ||||||||||||||||||||||
Db         45 AVNFQTGFSGNDIAFHFNPRFE 66


RESULT 5
LEG9_RAT
ID   LEG9_RAT       STANDARD;      PRT;   354 AA.
AC   P97840; O08588; O35866;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-9 (36 kDa beta-galactoside binding lectin) (Urate
DE   transporter/channel) (UAT).
GN   Name=Lgals9;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney, and Small intestine;
RX   MEDLINE=97190351; PubMed=9038233; DOI=10.1074/jbc.272.9.6078;
RA   Wada J., Kanwar Y.S.;
RT   "Identification and characterization of galectin-9, a novel beta-
RT   galactoside-binding mammalian lectin.";
RL   J. Biol. Chem. 272:6078-6086(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM SHORT).
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX   MEDLINE=97150769; PubMed=8995305; DOI=10.1074/jbc.272.1.617;
RA   Leal-Pinto E., Tao W., Rappaport J., Richardson M., Knorr B.A.,
RA   Abramson R.G.;
RT   "Molecular cloning and functional reconstitution of a urate
RT   transporter/channel.";
RL   J. Biol. Chem. 272:617-625(1997).
CC   -!- FUNCTION: Binds galactosides. May play a role in thymocyte-
CC       epithelial interactions relevant to the biology of the thymus (By
CC       similarity). May provide the molecular basis for urate flux across
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CC       cell membranes, allowing urate that is formed during purine
CC       metabolism to efflux from cells and serving as an electrogenic
CC       transporter that plays an important role in renal and
CC       gastrointestinal urate excretion. Highly selective to the anion
CC       urate.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. May also be secreted by a non-
CC       classical secretory pathway (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=Long;
CC         IsoId=P97840-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=P97840-2; Sequence=VSP_003098;
CC   -!- TISSUE SPECIFICITY: The long form is expressed exclusively in the
CC       small intestine.
CC   -!- DOMAIN: Contains two homologous but distinct carbohydrate-binding
CC       domains.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U59462; AAB51192.1; -.
DR   EMBL; U72741; AAB68592.1; -.
DR   EMBL; U67958; AAB48591.1; -.
DR   HSSP; P17931; 1A3K.
DR   RGD; 3005; Lgals9.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Alternative splicing; Galectin; Ion transport; Lectin; Repeat.
FT   DOMAIN        1    147       Galaptin 1.
FT   DOMAIN      148    205       Linker.
FT   DOMAIN      206    354       Galaptin 2.
FT   SITE         81     87       Beta-galactoside binding 1 (By
FT                                similarity).
FT   SITE        286    292       Beta-galactoside binding 2 (By
FT                                similarity).
FT   VARSPLIC    148    179       Missing (in isoform Short).
FT                                /FTId=VSP_003098.
SQ   SEQUENCE   354 AA;  39946 MW;  6574F960B2EAF37C CRC64;

  Query Match             7.1%;  Score 22;  DB 1;  Length 354;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-14;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 AVNFQTGFSGNDIAFHFNPRFE 67
              ||||||||||||||||||||||
Db         45 AVNFQTGFSGNDIAFHFNPRFE 66


RESULT 6
LEG5_RAT
ID   LEG5_RAT       STANDARD;      PRT;   144 AA.
AC   P47967;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-5 (RL-18).
GN   Name=Lgals5;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Reticulocytes;
RX   MEDLINE=95197487; PubMed=7890611; DOI=10.1074/jbc.270.10.5032;
RA   Gitt M.A., Wiser M.F., Leffler H., Herrmann J., Xia Y.-R., Massa S.M.,
RA   Cooper D.N.W., Lusis A.J., Barondes S.H.;
RT   "Sequence and mapping of galectin-5, a beta-galactoside-binding
RT   lectin, found in rat erythrocytes.";
RL   J. Biol. Chem. 270:5032-5038(1995).
CC   -!- FUNCTION: May function in erythrocyte differentiation.
CC   -!- SUBUNIT: Monomer.
CC   -!- TISSUE SPECIFICITY: Erythrocytes.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L36862; AAC42050.1; -.
DR   EMBL; L21711; AAA65445.1; -.
DR   PIR; A55932; A55932.
DR   HSSP; P47929; 1BKZ.
DR   RGD; 3004; Lgals5.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 1.
DR   SMART; SM00276; GLECT; 1.
DR   PROSITE; PS00309; GALAPTIN; 1.
KW   Acetylation; Direct protein sequencing; Galectin; Lectin.
FT   INIT_MET      0      0
FT   SITE         76     82       Beta-galactoside binding (Potential).
FT   MOD_RES       1      1       N-acetylserine.
FT   CONFLICT    127    135       Missing (in Ref. 1; AAA65445).
SQ   SEQUENCE   144 AA;  16065 MW;  BC95283D760DA515 CRC64;

  Query Match             6.4%;  Score 20;  DB 1;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        220 IAFHLNPRFDENAVVRNTQI 239
              ||||||||||||||||||||
Db         53 IAFHLNPRFDENAVVRNTQI 72


RESULT 7
Q6QZP2
ID   Q6QZP2      PRELIMINARY;      PRT;   323 AA.
AC   Q6QZP2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Galectin 9.
GN   Name=UAT;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bannasch D.L., Ryun J.R., Bannasch M.J., Schaible R.H., Breen M.,
RA   Ling G.;
RT   "Exclusion of galectin 9 as a candidate gene for hyperuricosuria in
RT   the Dalmatian dog.";
RL   Anim. Genet. 35:326-328(2004).
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; AY521549; AAS80311.1; -.
DR   HSSP; P17931; 1A3K.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
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DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Galectin; Lectin.
SQ   SEQUENCE   323 AA;  36026 MW;  2C4FA3644A0EB64F CRC64;

  Query Match             5.5%;  Score 17;  DB 2;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-09;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        241 NSWGSEERSLPRKMPFV 257
              |||||||||||||||||
Db        253 NSWGSEERSLPRKMPFV 269


RESULT 8
Q9XSM8
ID   Q9XSM8      PRELIMINARY;      PRT;   317 AA.
AC   Q9XSM8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Urate transporter/channel protein (UATp).
GN   Name=uatp;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=21554766; PubMed=11698107; DOI=10.1016/S0300-9084(01)01335-9;
RA   Spitzenberger F., Graessler J., Schroeder H.E.;
RT   "Molecular and functional characterization of galectin 9 mRNA isoforms
RT   in porcine and human cells and tissues.";
RL   Biochimie 83:851-862(2001).
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; AJ131826; CAB44278.1; -.
DR   HSSP; P11116; 1SLT.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 1.
KW   Galectin; Lectin.
SQ   SEQUENCE   317 AA;  35342 MW;  AA09562C4B7B8B80 CRC64;

  Query Match             5.1%;  Score 16;  DB 2;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        274 KVAVDGQHLFEYYHRL 289
              ||||||||||||||||
Db        286 KVAVDGQHLFEYYHRL 301


RESULT 9
Q9XSM9
ID   Q9XSM9      PRELIMINARY;      PRT;   349 AA.
AC   Q9XSM9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Urate transporter/channel protein, isoform (UATp,i).
GN   Name=uatp.i;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=21554766; PubMed=11698107; DOI=10.1016/S0300-9084(01)01335-9;
RA   Spitzenberger F., Graessler J., Schroeder H.E.;
RT   "Molecular and functional characterization of galectin 9 mRNA isoforms
RT   in porcine and human cells and tissues.";
RL   Biochimie 83:851-862(2001).
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; AJ131827; CAB44279.1; -.
DR   HSSP; P11116; 1SLT.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 1.
KW   Galectin; Lectin.
SQ   SEQUENCE   349 AA;  38899 MW;  BF83D3E213E7B64C CRC64;

  Query Match             5.1%;  Score 16;  DB 2;  Length 349;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        274 KVAVDGQHLFEYYHRL 289
              ||||||||||||||||
Db        318 KVAVDGQHLFEYYHRL 333


RESULT 10
Q99L83
ID   Q99L83      PRELIMINARY;      PRT;   322 AA.
AC   Q99L83;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Lgals9 protein.
GN   Name=Lgals9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; BC003754; AAH03754.1; -.
DR   HSSP; P17931; 1A3K.
DR   MGD; MGI:109496; Lgals9.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
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DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Galectin; Lectin.
SQ   SEQUENCE   322 AA;  36545 MW;  032D77400737562E CRC64;

  Query Match             4.2%;  Score 13;  DB 2;  Length 322;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRFE 67
              |||||||||||||
Db         54 GNDIAFHFNPRFE 66


RESULT 11
LEG9_MOUSE
ID   LEG9_MOUSE     STANDARD;      PRT;   353 AA.
AC   O08573; O08572;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-9.
GN   Name=Lgals9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD-1; TISSUE=Kidney, and Small intestine;
RX   MEDLINE=97190351; PubMed=9038233; DOI=10.1074/jbc.272.9.6078;
RA   Wada J., Kanwar Y.S.;
RT   "Identification and characterization of galectin-9, a novel beta-
RT   galactoside-binding mammalian lectin.";
RL   J. Biol. Chem. 272:6078-6086(1997).
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=97298141; PubMed=9153289;
RA   Wada J., Ota K., Kumar A., Wallner E.I., Kanwar Y.S.;
RT   "Developmental regulation, expression, and apoptotic potential of
RT   galectin-9, a beta-galactoside binding lectin.";
RL   J. Clin. Invest. 99:2452-2461(1997).
CC   -!- FUNCTION: Binds galactosides. May play a role in thymocyte-
CC       epithelial interactions relevant to the biology of the thymus.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic. May also be secreted by a non-
CC       classical secretory pathway.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=Long;
CC         IsoId=O08573-1; Sequence=Displayed;
CC       Name=Short;
CC         IsoId=O08573-2; Sequence=VSP_003097;
CC   -!- TISSUE SPECIFICITY: Accentuated expression in liver and thymus of
CC       embryo, detected in embryonic heart, brain, lung, liver, and
CC       kidney. Highly expressed in adult thymus, small intestine, and
CC       liver, and to a lesser extent in lung, kidney, spleen, cardiac,
CC       and skeletal muscle. Barely detectable in brain and reticulocyte.
CC       The long form is expressed exclusively in the small intestine.
CC   -!- DEVELOPMENTAL STAGE: The expression increased with successive
CC       stages of embryonic development.
CC   -!- DOMAIN: Contains two homologous but distinct carbohydrate-binding
CC       domains.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U55061; AAB51190.1; -.
DR   EMBL; U55060; AAB51189.1; -.
DR   HSSP; P17931; 1A3K.
DR   MGD; MGI:109496; Lgals9.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   PROSITE; PS00309; GALAPTIN; 2.
KW   Alternative splicing; Galectin; Lectin; Repeat.
FT   DOMAIN       1    147       Galaptin 1.
FT   DOMAIN     148    204       Linker.
FT   DOMAIN     205    353       Galaptin 2.
FT   SITE        81     87       Beta-galactoside binding 1 (By
FT                               similarity).
FT   SITE       285    291       Beta-galactoside binding 2 (By
FT                               similarity).
FT   VARSPLIC   148    178       Missing (in isoform Short).
FT                               /FTId=VSP_003097.
SQ   SEQUENCE   353 AA;  40036 MW;  B54036F6E280C531 CRC64;

  Query Match             4.2%;  Score 13;  DB 1;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRFE 67
              |||||||||||||
Db         54 GNDIAFHFNPRFE 66


RESULT 12
LEG3_CRILO
ID   LEG3_CRILO     STANDARD;      PRT;   244 AA.
AC   P47953;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding
DE   protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE   (Laminin-binding protein) (Lectin L-29) (CBP30).
GN   Name=LGALS3;
OS   Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Cricetulus.
OX   NCBI_TaxID=10030;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=94299546; PubMed=8027086;
RA   Mehul B., Bawumia S., Martin S.R., Hughes R.C.;
RT   "Structure of baby hamster kidney carbohydrate-binding protein CBP30,
RT   an S-type animal lectin.";
RL   J. Biol. Chem. 269:18250-18258(1994).
CC   -!- FUNCTION: Galactose-specific lectin which binds IgE.
CC   -!- SIMILARITY: In the C-terminal section; belongs to the galectin
CC       (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X78879; CAA55479.1; -.
DR   HSSP; P17931; 1A3K.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 1.
DR   PROSITE; PS00309; GALAPTIN; 1.
```

```
KW   Acetylation; Galectin; IgE-binding protein; Lectin; Phosphorylation;
KW   Repeat.
FT   INIT_MET      0      0       By similarity.
FT   SITE        175    181       Beta-galactoside binding (By similarity).
FT   MOD_RES       1      1       N-acetylalanine (By similarity).
FT   MOD_RES       5      5       Phosphoserine (by CK1) (By similarity).
FT   DOMAIN       34     98       7 X 9 AA tandem repeats of Y-P-G-X(3)-P-
FT                                [GS]-A.
FT   REPEAT       34     42       1.
FT   REPEAT       43     51       2.
FT   REPEAT       52     60       3.
FT   REPEAT       61     69       4.
FT   REPEAT       70     77       5 (approximate).
FT   REPEAT       78     87       6 (approximate).
FT   REPEAT       88     98       7 (approximate).
FT   DOMAIN      112    244       Galaptin.
FT   DISULFID    167    167       Interchain (By similarity).
SQ   SEQUENCE   244 AA;  25608 MW;  8F99B9AA0BBA7D3F CRC64;

  Query Match             3.9%;  Score 12;  DB 1;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRF 66
              ||||||||||||
Db        146 GNDIAFHFNPRF 157


RESULT 13
LEG3_RAT
ID   LEG3_RAT       STANDARD;      PRT;   261 AA.
AC   P08699;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding
DE   protein) (35 kDa lectin) (Carbohydrate binding protein 35) (CBP 35)
DE   (Laminin-binding protein) (Lectin L-29).
GN   Name=Lgals3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88016189; PubMed=2958848;
RA   Albrandt K., Orida N.K., Liu F.-T.;
RT   "An IgE-binding protein with a distinctive repetitive sequence and
RT   homology with an IgG receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:6859-6863(1987).
RN   [2]
RP   SEQUENCE OF 124-261 FROM N.A.
RX   MEDLINE=85216641; PubMed=3858867;
RA   Liu F.-T., Albrandt K., Mendel E., Kulczycki A. Jr., Orida N.K.;
RT   "Identification of an IgE-binding protein by molecular cloning.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:4100-4104(1985).
RN   [3]
RP   SEQUENCE OF 119-144.
RX   MEDLINE=90105471; PubMed=2605254;
RA   Lefler H., Masiarz F.R., Barondes S.H.;
RT   "Soluble lactose-binding vertebrate lectins: a growing family.";
RL   Biochemistry 28:9222-9229(1989).
RN   [4]
RP   PARTIAL SEQUENCE, AND ACETYLATION.
RX   MEDLINE=94075368; PubMed=8253805;
RA   Herrmann J., Turck C.W., Atchison R.E., Huflejt M.E., Poulter L.,
RA   Gitt M.A., Burlingame A.L., Barondes S.H., Leffler H.;
RT   "Primary structure of the soluble lactose binding lectin L-29 from rat
RT   and dog and interaction of its non-collagenous proline-, glycine-,
RT   tyrosine-rich sequence with bacterial and tissue collagenase.";
RL   J. Biol. Chem. 268:26704-26711(1993).
CC   -!- FUNCTION: Galactose-specific lectin which binds IgE.
CC   -!- SUBUNIT: Probably forms homo- or heterodimers. Binds LGALS3BP (By
CC       similarity).
CC   -!- SIMILARITY: In the C-terminal section; belongs to the galectin
CC       (galaptin/S-lectin) family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J02962; AAA40828.1; -.
DR   EMBL; M13697; AAA41378.1; -.
DR   PIR; A54889; A54889.
DR   HSSP; P17931; 1A3K.
DR   RGD; 69356; Lgals3.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 1.
DR   PROSITE; PS00309; GALAPTIN; 1.
KW   Acetylation; Direct protein sequencing; Galectin; IgE-binding protein;
KW   Lectin; Phosphorylation; Repeat.
FT   INIT_MET      0      0
FT   SITE        192    198       Beta-galactoside binding (By similarity).
FT   MOD_RES       1      1       N-acetylalanine.
FT   MOD_RES       5      5       Phosphoserine (by CK1) (By similarity).
FT   DOMAIN       34    111       9 X 9 AA tandem repeats of Y-P-G-X(3)-P-
FT                                [GS]-[AG].
FT   REPEAT       34     42       1.
FT   REPEAT       43     51       2.
FT   REPEAT       52     60       3.
FT   REPEAT       61     69       4.
FT   REPEAT       70     78       5.
FT   REPEAT       79     87       6.
FT   REPEAT       88     97       7 (approximate).
FT   REPEAT       98    104       8 (approximate).
FT   REPEAT      105    111       9 (incomplete).
FT   DOMAIN      129    261       Galaptin.
FT   DISULFID    184    184       Interchain (By similarity).
FT   CONFLICT     19     19       Q -> R (in Ref. 1).
SQ   SEQUENCE   261 AA;  27070 MW;  EAFA117F5EA5080D CRC64;

  Query Match             3.9%;  Score 12;  DB 1;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.0012;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRF 66
              ||||||||||||
Db        163 GNDIAFHFNPRF 174


RESULT 14
Q8UW97
ID   Q8UW97       PRELIMINARY;      PRT;   332 AA.
AC   Q8UW97;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Galectin family xgalectin-IVa.
GN   Name=xgalectin-IVa;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=21968527; PubMed=11971860; DOI=10.1093/glycob/12.3.163;
RA   Shoji H., Nishi N., Hirashima M., Nakamura T.;
RT   "Purification and cDNA cloning of Xenopus liver galectins and their
RT   expression.";
```

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RL   Glycobiology 12:163-172(2002).
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; AB060972; BAB83259.1; -.
DR   HSSP; P17931; 1A3K.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
KW   Galectin; Lectin.
SQ   SEQUENCE   332 AA;  36822 MW;  D273F8D35484E9C2 CRC64;

  Query Match             3.5%;  Score 11;  DB 2;  Length 332;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 NDIAFHFNPRF 66
              ||||||||||| 
Db         50 NDIAFHFNPRF 60


RESULT 15
Q6PGR5
ID   Q6PGR5      PRELIMINARY;      PRT;   353 AA.
AC   Q6PGR5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Xgalectin-iva protein (Fragment).
GN   Name=xgalectin-iva;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the galectin (galaptin/S-lectin) family.
DR   EMBL; BC056859; AAH56859.1; -.
DR   HSSP; P17931; 1A3K.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR008985; ConA_like_lec_gl.
DR   InterPro; IPR001079; Galectin.
DR   Pfam; PF00337; Gal-bind_lectin; 2.
DR   SMART; SM00276; GLECT; 2.
KW   Galectin; Lectin.
FT   NON_TER       1      1
SQ   SEQUENCE   353 AA;  39242 MW;  0453CD44E93DB1C6 CRC64;

  Query Match             3.5%;  Score 11;  DB 2;  Length 353;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 NDIAFHFNPRF 66
              ||||||||||| 
Db         71 NDIAFHFNPRF 81


Search completed: July 13, 2005, 08:01:45
Job time : 177 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 163 Seconds
(without alignments)
737.929 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 311

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	311	100.0	311	2	AAW56504	Aaw56504 Human gal
2	306	98.4	311	5	ABB77854	Abb77854 Amino aci
3	163	52.4	233	8	ADP81097	Adp81097 Protein o
4	163	52.4	323	3	AAY56802	Aay56802 Human eos
5	163	52.4	323	5	ABB77853	Abb77853 Amino aci
6	163	52.4	323	5	ABP61494	Abp61494 Human NF-
7	163	52.4	323	8	ADQ66730	Adq66730 Novel hum
8	163	52.4	355	2	AAY06997	Aay06997 Galectin-
9	163	52.4	355	2	AAW85664	Aaw85664 Galectin-
10	163	52.4	355	5	ABB77852	Abb77852 Amino aci
11	163	52.4	355	7	ADC53845	Adc53845 Human gal
12	163	52.4	355	7	ADE62929	Ade62929 Human Pro
13	163	52.4	355	7	ADD48101	Add48101 Human Pro
14	163	52.4	355	7	ADG91608	Adg91608 Human lec
15	163	52.4	378	4	AAE13847	Aae13847 Human lun
16	163	52.4	378	7	ADD66747	Add66747 Human lun
17	163	52.4	378	7	ADE88001	Ade88001 Human lun
18	148	47.6	168	3	AAB11899	Aab11899 Human col
19	148	47.6	168	4	AAM24496	Aam24496 Colon tum
20	148	47.6	168	6	ABP55345	Abp55345 Human col
21	148	47.6	301	7	ABU63651	Abu63651 Human ura
22	87	28.0	323	8	ADP12958	Adp12958 Protein e
23	73	23.5	246	6	ABU69164	Abu69164 Human NOV
24	73	23.5	246	8	ADO08331	Ado08331 Human NOV
25	69	22.2	145	2	AAW61613	Aaw61613 Human gal
26	69	22.2	149	2	AAW61614	Aaw61614 Human gal
27	41	13.2	355	6	ABU69163	Abu69163 Human NOV
28	41	13.2	355	8	ADO08329	Ado08329 Human NOV
29	38	12.2	97	3	AAB43992	Aab43992 Human can
30	29	9.3	757	4	ABG06703	Abg06703 Novel hum
31	22	7.1	322	7	ABU63650	Abu63650 Rat urate
32	22	7.1	354	7	ADC53848	Adc53848 Rat galec
33	22	7.1	354	7	ADE62927	Ade62927 Rat Prote
34	22	7.1	354	7	ADD48099	Add48099 Rat Prote
35	20	6.4	144	7	ADE57164	Ade57164 Rat Prote
36	20	6.4	144	7	ADE57162	Ade57162 Rat Prote
37	20	6.4	145	7	ABW01522	Abw01522 Protein #
38	20	6.4	145	7	ADG40248	Adg40248 Rat galec
39	17	5.5	17	5	ABB77857	Abb77857 Amino aci
40	17	5.5	29	5	ABB77856	Abb77856 Amino aci
41	17	5.5	61	5	ABB77855	Abb77855 Amino aci
42	16	5.1	329	5	AAU97036	Aau97036 Human bla
43	13	4.2	322	7	ADC53842	Adc53842 Mouse gal
44	12	3.9	138	1	AAP60534	Aap60534 C-termina
45	12	3.9	245	8	ADN17285	Adn17285 Hamster g

ALIGNMENTS

RESULT 1
AAW56504
ID AAW56504 standard; protein; 311 AA.
XX
AC AAW56504;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human galectin 9.
XX
KW Galectin 9; lectin; human; autoimmune disease; inflammatory disease;
KW asthma; allergy; melanoma; renal astrocytoma; Hodgkin disease;
KW breast cancer; ovary cancer; prostate cancer; bone cancer; liver cancer;
KW lung cancer; pancreas cancer; spleen cancer; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 62. .102
FT /note= "antigenic region"
FT Region 197. .308
FT /note= "antigenic region"
FT Region 226. .259
FT /note= "antigenic region"
XX
PN WO9815624-A1.
XX
PD 16-APR-1998.
XX
PF 09-OCT-1997; 97WO-US018261.
XX
PR 09-OCT-1996; 96US-0028093P.
PR 09-OCT-1996; 96WO-US016565.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Gentz RL, Ruben SM;
XX
DR WPI; 1998-240812/21.
DR N-PSDB; AAV29786.
XX
PT Galectin 8, 9, 10 and 10SV polynucleotides - used for treating cancer,
PT autoimmune diseases, inflammatory diseases, asthma, and allergic
PT diseases.
XX
PS Claim 9; Fig 2A-B; 118pp; English.
XX
CC This polypeptide comprises novel human galectin 9. Its amino acid

```
CC   sequence was deduced from a human adult pancreatic tumour cDNA clone (see
CC   AAV29786). Novel galectins 8, 9, 10 and 10 splice variant (10SV) are
CC   claimed (see AAW56503-06). These can be obtained using a claimed method
CC   by expression in recombinant host cells. The novel galectins are used in
CC   a claimed method for treating a cell growth disorder, especially cancer,
CC   autoimmune diseases, inflammatory diseases, asthma, and allergic
CC   diseases, in a mammal. They are especially useful for diagnosis of
CC   melanoma, renal astrocytoma, Hodgkin disease, and breast, ovarian,
CC   prostate, bone, liver, lung, pancreatic and splenic cancers. The
CC   invention further relates to screening methods for identifying agonists
CC   and antagonists of galectin 8, 9, 20 or 10SV activity, and to diagnostic
CC   methods involving estimating levels of galectin 8, 9, 10 or 10SV protein
CC   or mRNA
XX
SQ   Sequence 311 AA;

  Query Match             100.0%;  Score 311;  DB 2;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-305;
  Matches  311;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

Qy         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120

Qy        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QYFHRVPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYP 180

Qy        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQID 240

Qy        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEV 300

Qy        301 GGDIQLTHVQT 311
              |||||||||||
Db        301 GGDIQLTHVQT 311


RESULT 2
ABB77854
ID   ABB77854 standard; protein; 311 AA.
XX
AC   ABB77854;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Amino acid sequence of a human protein.
XX
KW   Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
KW   ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
KW   kidney cancer; thyroid cancer; throat cancer; tongue cancer;
KW   upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
KW   lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
KW   leukemia; liposarcoma; glioma.
XX
OS   Homo sapiens.
XX
PN   WO200237114-A1.
XX
PD   10-MAY-2002.
XX
PF   31-OCT-2001; 2001WO-JP009561.
XX
PR   01-NOV-2000; 2000JP-00335077.
XX
PA   (GALP-) GALPHARMA CO LTD.
XX
PI   Hirashima M,  Yamauchi A,  Kageshita T,  Nakamura T,  Nishi N;
XX
DR   WPI; 2002-519265/55.
XX
PT   Metastasis mechanism-based agents (anti-galectin 9 antibody) for
PT   detecting ability of cancer to metastasize in cells, uses galectin 9 as
PT   marker to detect cancer metastasis for diagnosis, cancer prevention and
PT   treatment.
XX
PS   Disclosure; Page 63-64; 68pp; Japanese.
XX
CC   The specification describes an agent for detecting the ability of cancers
CC   to metastasize. This agents an comprises anti-galectin 9 antibody as the
CC   active ingredient. The agents and method are for or detecting ability of
CC   cancer to metastasize in cancer cells, which are useful in the diagnosis,
CC   prevention and treatment of cancer. The cancer includes epithelial
CC   malignant tumours (tumorising or non-tumorising) in organs, tissues or
CC   blood. Such cancer can be 1 of the not less than 31 specifically claimed,
CC   e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
CC   uterus cancer, malignant tumour of the testis, prostate cancer, bladder
CC   cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,
CC   tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
CC   and rectum cancer, lung and bronchus cancer, liver cancer (including
CC   hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
CC   duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
CC   lymphoma, liposarcoma and glioma. The cancer cells are particularly
CC   breast cancer cells or melanoma cells. The present sequence represents a
CC   human protein, which is used in the course of the invention
XX
SQ   Sequence 311 AA;

  Query Match             98.4%;  Score 306;  DB 5;  Length 311;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-300;
  Matches  306;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 SQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPR 65
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 SQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAFHFNPR 65

Qy         66 FEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHR 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 FEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHR 125

Qy        126 VPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFIT 185
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 VPFHRVDTISVNGSVQLSYISFQTQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFIT 185

Qy        186 TILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGS 245

Qy        246 EERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQ 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 EERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQ 305

Qy        306 LTHVQT 311
              ||||||
Db        306 LTHVQT 311


RESULT 3
ADP81097
ID   ADP81097 standard; protein; 233 AA.
XX
AC   ADP81097;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Protein of human ovarian specific gene, SEQ ID No 131.
XX
KW   normal; neoplastic; ovarian; ovarian specific nucleic acid; OSNA;
KW   metastatic; cancer; vaccine; cytostatic; human.
```

XX
OS Homo sapiens.
XX
PN WO2004053079-A2.
XX
PD 24-JUN-2004.
XX
PF 08-DEC-2003; 2003WO-US038855.
XX
PR 06-DEC-2002; 2002US-0431301P.
PR 06-DEC-2002; 2002US-0431321P.
PR 30-JUN-2003; 2003US-0484584P.
PR 07-NOV-2003; 2003US-0518607P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Macina RA, Turner LR, Sun Y, Liu S, Chen H;
XX
DR WPI; 2004-468850/44.
DR N-PSDB; ADP80968.
XX
PT New ovarian specific nucleic acid molecules and polypeptides useful for
PT diagnosing, preventing or treating ovarian cancer, for producing
PT transgenic animals or cells, or for research purposes.
XX
PS Claim 12; SEQ ID NO 131; 754pp; English.
XX
CC The invention relates to novel isolated nucleic acid molecules and
CC polypeptides present in normal and neoplastic ovarian cells. These
CC comprise a nucleic acid sequence encoding any of the 167 amino acid
CC sequences (e.g. 438, 237 or 233 amino acids) fully defined in the
CC specification (SEQ. ID NOs: ADP81095 to ADP81261) and comprises any of
CC the 128 nucleotide sequences (e.g. 4798, 1494 or 1691 bp) fully defined
CC in the specification (SEQ. ID NOs: ADP80967 to ADP81094). The invention
CC further comprises: a method for determining the presence of a ovarian
CC specific nucleic acid (OSNA) in a sample; a vector comprising the above
CC nucleic acid molecule; a host cell comprising the vector; a method for
CC producing a polypeptide encoded by the above nucleic acid molecule; a
CC polypeptide encoded by the nucleic acid molecule cited above; an antibody
CC or its fragment that specifically binds to the above polypeptide; a
CC method for determining the presence of an ovarian specific protein in a
CC sample; a method for diagnosing or monitoring the presence and metastases
CC of ovarian cancer in a patient; a kit for detecting a risk of cancer or
CC presence of cancer in a patient, the kit comprising a means for
CC determining the presence of the above nucleic acid molecule or
CC polypeptide; a method of treating a patient with ovarian cancer; and a
CC vaccine comprising the above polypeptide or nucleic acid encoding the
CC polypeptide. The isolated nucleic acid molecules and polypeptides have
CC cytostatic activity. The isolated polypeptides may be used to create a
CC vaccine. The isolated nucleic acid molecules and polypeptides can be used
CC for diagnosing or monitoring the presence and metastases of ovarian
CC cancer and treating ovarian cancer. This sequence represents the protein
CC of an ovarian specific gene of the invention.
XX
SQ Sequence 233 AA;

Query Match 52.4%; Score 163; DB 8; Length 233;
Best Local Similarity 100.0%; Pred. No. 8.7e-156;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 71 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 130

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 131 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 190

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 191 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 233

RESULT 4
AAY56802
ID AAY56802 standard; protein; 323 AA.
XX
AC AAY56802;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human eosinophil chemotactic factor (ecalectin).
XX
KW Eosinophil chemotactic factor; galectin; chemotaxis inhibitor;
KW inflammatory disorder; eosinophil; allergic disease; asthma; human;
KW allergic rhinitis; atopic dermatitis; ecalectin; galectin.
XX
OS Homo sapiens.
XX
PN WO9962556-A1.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-JP002952.
XX
PR 03-JUN-1998; 98JP-00170698.
XX
PA (EFFE-) EFFECTOR CELL INST.
XX
PI Kanegasaki S, Matsumoto R, Hirashima M;
XX
DR WPI; 2000-086860/07.
DR N-PSDB; AAZ46748.
XX
PT Ecalectin and other galectins as eosinophil chemotaxis promoters for
PT screening potential inhibitors of this effect.
XX
PS Disclosure; Page 35-39; 49pp; Japanese.
XX
CC The invention provides compositions for increasing the chemotacticity of
CC eosinophils that contain as active component a galectin. Chemotaxis
CC inhibitors identified by the screening are used as agents for the
CC treatment and prevention of inflammatory disorders caused by the increase
CC of eosinophil content in affected tissues, such as allergic diseases
CC including bronchial asthma, allergic rhinitis and atopic dermatitis. The
CC present sequence represents a human eosinophil chemotactic factor,
CC ecalectin. Ecalectin belongs to the family of galectin and has eosinophil
CC chemotactic activity
XX
SQ Sequence 323 AA;

Query Match 52.4%; Score 163; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323

RESULT 5
ABB77853
ID ABB77853 standard; protein; 323 AA.
XX
AC ABB77853;
XX
DT 27-SEP-2002 (first entry)
XX

DE Amino acid sequence of a human protein.
XX
KW Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;
KW upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
KW leukemia; liposarcoma; glioma.
XX
OS Homo sapiens.
XX
PN WO200237114-A1.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-JP009561.
XX
PR 01-NOV-2000; 2000JP-00335077.
XX
PA (GALP-) GALPHARMA CO LTD.
XX
PI Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;
XX
DR WPI; 2002-519265/55.
XX
PT Metastasis mechanism-based agents (anti-galectin 9 antibody) for
PT detecting ability of cancer to metastasize in cells, uses galectin 9 as
PT marker to detect cancer metastasis for diagnosis, cancer prevention and
PT treatment.
XX
PS Example 5; Page 61-63; 68pp; Japanese.
XX
CC The specification describes an agent for detecting the ability of cancers
CC to metastasize. This agents an comprises anti-galectin 9 antibody as the
CC active ingredient. The agents and method are for or detecting ability of
CC cancer to metastasize in cancer cells, which are useful in the diagnosis,
CC prevention and treatment of cancer. The cancer includes epithelial
CC malignant tumours (tumorising or non-tumorising) in organs, tissues or
CC blood. Such cancer can be 1 of the not less than 31 specifically claimed,
CC e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder
CC cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,
CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
CC and rectum cancer, lung and bronchus cancer, liver cancer (including
CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
CC lymphoma, liposarcoma and glioma. The cancer cells are particularly
CC breast cancer cells or melanoma cells. The present sequence represents a
CC human protein, which is used in the course of the invention
XX
SQ Sequence 323 AA;

Query Match 52.4%; Score 163; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy      209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy      269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
            |||||||||||||||||||||||||||||||||||||||||||
Db      281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323
```

RESULT 6
ABP61494
ID ABP61494 standard; protein; 323 AA.
XX
AC ABP61494;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human NF-kB activating protein SEQ ID NO 141.
XX
KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
XX
OS Homo sapiens.
XX
PN WO200253737-A1.
XX
PD 11-JUL-2002.
XX
PF 25-DEC-2001; 2001WO-JP011389.
XX
PR 28-DEC-2000; 2000JP-00402288.
PR 26-MAR-2001; 2001JP-00088912.
PR 24-AUG-2001; 2001JP-00254018.
XX
PA (ASAH) ASAHI KASEI KOGYO KK.
XX
PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX
DR WPI; 2002-583617/62.
DR N-PSDB; ABQ91982.
XX
PT NF-approximatelykB activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer.
XX
PS Claim 1; Page 613-615; 841pp; Japanese.
XX
CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition and
CC for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders
XX
SQ Sequence 323 AA;

Query Match 52.4%; Score 163; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy      209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy      269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
            |||||||||||||||||||||||||||||||||||||||||||
Db      281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323
```

RESULT 7
ADQ66730
ID ADQ66730 standard; protein; 323 AA.
XX
AC ADQ66730;
XX
DT 07-OCT-2004 (first entry)

XX
DE Novel human protein sequence #1703.
XX
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
OS Homo sapiens.
XX
PN EP1440981-A2.
XX
PD 28-JUL-2004.
XX
PF 21-JAN-2004; 2004EP-00001196.
XX
PR 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX
DR WPI; 2004-535376/52.
DR N-PSDB; ADQ64542.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 3891; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
CC sequence of the invention.
XX
SQ Sequence 323 AA;

```
  Query Match             52.4%;  Score 163;  DB 8;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-155;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 220

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 280

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        281 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 323
```

RESULT 8
AAY06997
ID AAY06997 standard; protein; 355 AA.
XX
AC AAY06997;
XX
DT 02-JUL-1999 (first entry)
XX
DE Galectin-9 protein sequence.
XX
KW Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer.
XX
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US014679.
XX
PR 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX
DR WPI; 1999-132448/11.
DR N-PSDB; AAX40198.
XX
PT New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX
PS Example 8; Page 779-780; 787pp; English.
XX
CC The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the
CC interaction between the agent and the NAM or the expression product as a
CC determination of the disorder. The products and methods can be used in
CC the diagnosis, monitoring, research, or treatment of conditions
CC characterised by the expression of various cancer associated antigens.
CC The invention provides nucleic acid sequences and encoded polypeptides
CC which are cancer associated antigen precursors expressed in human breast
CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC lung cancer
XX
SQ Sequence 355 AA;

```
  Query Match             52.4%;  Score 163;  DB 2;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-155;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
```

RESULT 9
AAW85664
ID AAW85664 standard; protein; 355 AA.
XX
AC AAW85664;
XX
DT 19-JUL-1999 (first entry)
XX

DE Galectin-9 like protein.
XX
KW Galectin-9; lectin; galactose; Hodgkin's disease; pharmaceutical;
KW sugar chain; intercellular adhesion; cell proliferation.
XX
OS Homo sapiens.
XX
PN WO9910490-A1.
XX
PD 04-MAR-1999.
XX
PF 19-AUG-1998; 98WO-JP003670.
XX
PR 22-AUG-1997; 97JP-00226468.
XX
PA (SAGA) SAGAMI CHEM RES CENTRE.
PA (PROT-) PROTEGENE INC.
XX
PI Kato S, Yamaguchi T, Sekine S, Kamata K;
XX
DR WPI; 1999-228913/19.
DR N-PSDB; AAX08490, AAX08491.
XX
PT A new human protein having lactose binding properties.
XX
PS Claim 2; Page 55-57; 64pp; English.
XX
CC Galectins are the general term for animal lectins binding to galactose.
CC Animal lectins exist in many sites such as the cytoplasm, the nucleus,
CC the cell membrane etc. and are considered to be associated with cell
CC proliferation. Galectin-9 has been identified as an antigenic protein
CC reacting with an antibody contained in the serum of Hodgkin's disease and
CC has a structure where two sugar chain-binding domains are connected by a
CC linker peptide. The true role of galectin-9 in the body has not been
CC completely identified but is thought to be involved in intercellular
CC adhesion. The human galectin-9 like protein coding sequences are
CC characterised by containing the sequence described in AAX08489. The
CC protein can be used as pharmaceuticals or reagents for sugar chain
CC research. The cDNA is used as a probe for gene diagnosis and for gene
CC therapy
XX
SQ Sequence 355 AA;

Query Match 52.4%; Score 163; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355

RESULT 10
ABB77852
ID ABB77852 standard; protein; 355 AA.
XX
AC ABB77852;
XX
DT 27-SEP-2002 (first entry)
XX
DE Amino acid sequence of a human protein.
XX
KW Cancer; galectin 9; antibody; skin cancer; melanoma; breast cancer;
KW ovarian cancer; uterus cancer; tumour; prostate cancer; bladder cancer;
KW kidney cancer; thyroid cancer; throat cancer; tongue cancer;
KW upper jaw cancer; esophageal cancer; stomach cancer; colon cancer;
KW lung cancer; liver cancer; gall-bladder cancer; pancreatic cancer;
KW leukemia; liposarcoma; glioma.
XX
OS Homo sapiens.
XX
PN WO200237114-A1.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-JP009561.
XX
PR 01-NOV-2000; 2000JP-00335077.
XX
PA (GALP-) GALPHARMA CO LTD.
XX
PI Hirashima M, Yamauchi A, Kageshita T, Nakamura T, Nishi N;
XX
DR WPI; 2002-519265/55.
XX
PT Metastasis mechanism-based agents (anti-galectin 9 antibody) for
PT detecting ability of cancer to metastasize in cells, uses galectin 9 as
PT marker to detect cancer metastasis for diagnosis, cancer prevention and
PT treatment.
XX
PS Example 1; Page 60-61; 68pp; Japanese.
XX
CC The specification describes an agent for detecting the ability of cancers
CC to metastasize. This agents an comprises anti-galectin 9 antibody as the
CC active ingredient. The agents and method are for or detecting ability of
CC cancer to metastasize in cancer cells, which are useful in the diagnosis,
CC prevention and treatment of cancer. The cancer includes epithelial
CC malignant tumours (tumorising or non-tumorising) in organs, tissues or
CC blood. Such cancer can be 1 of the not less than 31 specifically claimed,
CC e.g. skin cancer (including melanoma), breast cancer, ovarian cancer,
CC uterus cancer, malignant tumour of the testis, prostate cancer, bladder
CC cancer, kidney cancer, thyroid cancer, cancer of throat and larynx,
CC tongue cancer, upper jaw cancer, esophageal cancer, stomach cancer, colon
CC and rectum cancer, lung and bronchus cancer, liver cancer (including
CC hepatocarcinoma and intrahepatic biliary cancer), extrahepatic biliary
CC duct and gall-bladder cancer, pancreatic cancer, leukemia, malignant
CC lymphoma, liposarcoma and glioma. The cancer cells are particularly
CC breast cancer cells or melanoma cells. The present sequence represents a
CC human protein, which is used in the course of the invention
XX
SQ Sequence 355 AA;

Query Match 52.4%; Score 163; DB 5; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355

RESULT 11
ADC53845
ID ADC53845 standard; protein; 355 AA.
XX
AC ADC53845;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human galectin 9 protein (long isoform).

XX
KW galectin-9; nephritis; glomerular nephritis; antiinflammatory;
KW glomerular infiltration; apoptosis; human.
XX
OS Homo sapiens.
XX
PN JP2002322082-A.
XX
PD 08-NOV-2002.
XX
PF 26-APR-2001; 2001JP-00129200.
XX
PR 26-APR-2001; 2001JP-00129200.
XX
PA (PROT-) PROTEGENE KK.
XX
DR WPI; 2003-367092/35.
XX
PT Agents for prevention and treatment of nephritis, comprise galectin-1,
PT galectin-3, or galectin-9, by inhibition of intraglomerular infiltration
PT of leukocytes, CD8 positive cells, and induction of apoptosis of CD8
PT positive cells.
XX
PS Disclosure; SEQ ID NO 4; 31pp; Japanese.
XX
CC This invention relates to the use of novel mammal derived galectin-1
CC (G1), -3 (G3) and -9 (G9) proteins as effective ingredients for
CC prevention and treatment of nephritis. The invention discloses agents for
CC prevention and treatment of nephritis, particularly glomerular nephritis
CC and may have antiinflammatory activities. The method of the invention
CC inhibits glomerular infiltration of leukocytes, CD8 positive cells and
CC apoptosis of CD8 positive cells. The method and sequences of the
CC invention may be used for prevention and treatment of nephritis,
CC particularly glomerular nephritis including inhibition of glomerular
CC infiltration of leukocytes, CD8 positive cells and apoptosis of CD8
CC positive cells. The present sequence represents the human galectin 9
CC protein (long isoform) used in the exemplification of the present
CC invention.
XX
SQ Sequence 355 AA;

Query Match 52.4%; Score 163; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355

RESULT 12
ADE62929
ID ADE62929 standard; protein; 355 AA.
XX
AC ADE62929;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein O00182, SEQ ID NO 8863.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.

XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; O00182.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates, its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 355 AA;

Query Match 52.4%; Score 163; DB 7; Length 355;
Best Local Similarity 100.0%; Pred. No. 1.3e-155;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy 209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy 269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
|||||||||||||||||||||||||||||||||||||||||||
Db 313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355

RESULT 13
ADD48101

```
ID   ADD48101 standard; protein; 355 AA.
XX
AC   ADD48101;
XX
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein O00182, SEQ ID NO 13799.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; O00182.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 355 AA;

  Query Match             52.4%;  Score 163;  DB 7;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-155;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
              |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 14
ADG91608
ID   ADG91608 standard; protein; 355 AA.
XX
AC   ADG91608;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human lectin galactoside binding protein (LGAL ) #2.
XX
KW   Human; lectin galactoside binding protein; LGAL; CHK pathway; cancer;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          16. .147
FT                   /note = Galactose binding lectin domain
FT   Domain          226. .335
FT                   /note = Galactose binding lectin domain
XX
PN   US2003165965-A1.
XX
PD   04-SEP-2003.
XX
PF   28-FEB-2003; 2003US-00376133.
XX
PR   01-MAR-2002; 2002US-0360757P.
XX
PA   (FRAN/) FRANCIS-LANG H.
PA   (NICO/) NICOLL M.
PA   (HEUE/) HEUER T S.
XX
PI   Francis-Lang H,  Nicoll M,  Heuer TS;
XX
DR   WPI; 2003-898058/82.
XX
PT   Identifying a candidate CHK pathway modulating agent for diagnosing or
PT   treating e.g. cancer by providing an assay system comprising lectin
PT   galactoside binding proteins and detecting a test agent-biased activity
PT   of the assay system.
XX
PS   Claim 13; SEQ ID NO 18; 34pp; English.
XX
CC   The invention relates to lectin galactoside binding proteins (LGALS) and
CC   their genes which are identified as modulators of the CHK pathway. It
CC   also relates to methods for identifying modulators of the CHK pathway.
CC   The method is useful for identifying a candidate CHK pathway modulating
CC   agent for preparing a composition for diagnosing or treating diseases
CC   e.g. cancer. The sequences of the invention are useful in gene therapy.
CC   The present sequence is human LGAL protein. This sequence is used to
CC   illustrate the method of the invention.
XX
SQ   Sequence 355 AA;

  Query Match             52.4%;  Score 163;  DB 7;  Length 355;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-155;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 252

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 312

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
                |||||||||||||||||||||||||||||||||||||||||||
Db        313 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355


RESULT 15
AAE13847
ID   AAE13847 standard; protein; 378 AA.
XX
AC   AAE13847;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human lung tumour-specific protein 21871.
XX
KW   Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
KW   antisense-therapy; vaccine; immune response; lung cancer; 21871.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 182. .183
FT                   /note= "Encoded by TTTCC"
XX
PN   WO200172295-A2.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US009991.
XX
PR   29-MAR-2000; 2000US-00538037.
PR   05-JUN-2000; 2000US-00588937.
PR   18-AUG-2000; 2000US-00640878.
PR   22-SEP-2000; 2000US-0234517P.
PR   01-NOV-2000; 2000US-00704512.
PR   14-DEC-2000; 2000US-00738973.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Reed SG,  Lodes MJ,  Mohamath R,  Secrist H,  Benson DR,  Indirias CY;
PI   Henderson RA,  Fling SP,  Algate PA,  Elliot M,  Mannion J,  Kalos MD;
XX
DR   WPI; 2001-639201/73.
DR   N-PSDB; AAD23459.
XX
PT   New human lung-specific polynucleotides and polypeptides for the
PT   diagnosis and treatment of disease e.g. lung cancer.
XX
PS   Disclosure; Page 331; 378pp; English.
XX
CC   The invention relates to isolated lung tumour-specific proteins and their
CC   corresponding cDNA molecules. Lung tumour-specific proteins and their
CC   antigen-presenting cells are useful for stimulating and/or expanding T
CC   cells specific for a tumour protein, and for inhibiting the development
CC   of cancer. The invention also relates to a composition useful for
CC   stimulating an immune response, and for treating cancer. The lung tumour
CC   specific oligonucleotide is useful in gene therapy and for diagnosis,
CC   detection and treatment of lung cancer. The present sequence is human
CC   lung tumour-specific protein
XX
SQ   Sequence 378 AA;

  Query Match            52.4%;  Score 163;  DB 4;  Length 378;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-155;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        149 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 208
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQ 275

Qy        209 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 268
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 RFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILC 335

Qy        269 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 311
                |||||||||||||||||||||||||||||||||||||||||||
Db        336 EAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 378


Search completed: July 13, 2005, 07:50:31
Job time : 167 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:46:47 ; Search time 40 Seconds
(without alignments)
748.085 Million cell updates/sec

Title: US-09-263-689-4
Perfect score: 311
Sequence: 1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 311

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	6.4	145	2	A55932	galectin-5 - rat
2	12	3.9	245	2	A54909	carbohydrate-bindi
3	12	3.9	262	2	A54889	IgE-binding protei
4	10	3.2	324	2	A46631	lactose-binding le
5	8	2.6	139	2	S08576	lectin - mouse (fr
6	8	2.6	242	2	JC4300	galectin-3 - rabbi
7	8	2.6	250	2	A35820	galectin 3 - human
8	8	2.6	264	2	A28651	galactose-specific
9	8	2.6	264	2	A45983	lactose-binding le
10	8	2.6	294	2	A49688	lactose-binding le
11	8	2.6	316	2	A55975	galectin-8 - rat
12	8	2.6	317	2	JC6147	prostate carcinoma
13	8	2.6	323	2	A55664	lectin L-36 - pig
14	8	2.6	881	2	AD2580	two component sens
15	8	2.6	881	2	C97362	protein sensor pro
16	8	2.6	1433	2	S54587	CAT8 protein - yea
17	7	2.3	161	2	S44757	ribosomal protein
18	7	2.3	169	1	S23478	probable benzoate
19	7	2.3	214	2	S21969	19K zein precursor
20	7	2.3	228	2	G95935	conserved hypothet
21	7	2.3	230	1	ZIZMA2	19K zein precursor
22	7	2.3	233	2	S47266	zein Zd1, 19K - ma
23	7	2.3	233	2	S15656	zein, 19K - maize
24	7	2.3	233	2	S47265	zein Zd1, 19K - ma
25	7	2.3	234	1	ZIZM3	19K zein precursor
26	7	2.3	235	2	S15655	zein, 19K - maize
27	7	2.3	269	2	G75148	hypothetical prote
28	7	2.3	279	2	T37216	beta-galactoside-b
29	7	2.3	285	2	T26325	hypothetical prote
30	7	2.3	296	2	A64110	cell division inhi
31	7	2.3	307	2	A28771	reaction center pr
32	7	2.3	308	1	WNRFMS	reaction center pr
33	7	2.3	308	2	T50761	reaction center pr
34	7	2.3	308	2	S24213	reaction center pr
35	7	2.3	310	2	AD2557	hypothetical prote
36	7	2.3	325	2	T50890	photosynthetic rea
37	7	2.3	325	2	F49964	photosynthetic rea
38	7	2.3	325	2	D95897	probable cellulase
39	7	2.3	327	2	G83551	hypothetical prote
40	7	2.3	331	2	S44962	lmbZ protein - Str
41	7	2.3	332	2	C96000	probable C4-dicarb
42	7	2.3	335	2	AI3111	hypothetical prote
43	7	2.3	335	2	D98175	hypothetical prote
44	7	2.3	344	2	T26901	hypothetical prote
45	7	2.3	345	2	C55741	thymopoietin gamma

ALIGNMENTS

RESULT 1
A55932
galectin-5 - rat
N;Alternate names: beta-galactoside binding lectin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A55932; PX0077
R;Gitt, M.A.; Wiser, M.F.; Leffler, H.; Herrmann, J.; Xia, Y.R.; Massa, S.M.; Cooper, D.
J. Biol. Chem. 270, 5032-5038, 1995
A;Title: Sequence and mapping of galectin-5, a beta-galactoside-binding lectin, found in
A;Reference number: A55932; MUID:95197487; PMID:7890611
A;Accession: A55932
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145 <GIT>
A;Cross-references: UNIPROT:P47967; GB:L36862; NID:g727175; PIDN:AAC42050.1; PID:g727176
R;Jung, S.K.; Fujimoto, D.
J. Biochem. 116, 547-553, 1994
A;Title: A novel beta-galactoside-binding lectin in adult rat kidney.
A;Reference number: PX0077; MUID:95155264; PMID:7852273
A;Accession: PX0077
A;Molecule type: protein
A;Residues: 7,'P',9-10,'T',12-19,'X',21-25;30-42;109-111,'N',113,'H',115,'VS',118-123,'K
A;Experimental source: kidney
C;Comment: This protein exhibits activity to various saccharides and binds to Engelbreth
C;Genetics:
A;Gene: LGALS5
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: acetylated amino end; lectin; monomer
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 6.4%; Score 20; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.7e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        220 IAFHLNPRFDENAVVRNTQI 239
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Db         54 IAFHLNPRFDENAVVRNTQI 73
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RESULT 2
A54909
carbohydrate-binding protein CBP30 - hamster
N;Alternate names: S-type animal lectin CBP30
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Aug-1999
C;Accession: A54909
R;Mehul, B.; Bawumia, S.; Martin, S.R.; Hughes, R.C.
J. Biol. Chem. 269, 18250-18258, 1994
A;Title: Structure of baby hamster kidney carbohydrate-binding protein CBP30, an S-type
A;Reference number: A54909; MUID:94299546; PMID:8027086
A;Accession: A54909

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-245 <MEH>
A;Cross-references: GB:X78879; NID:g535082; PIDN:CAA55479.1; PID:g535083
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin

  Query Match             3.9%;  Score 12;  DB 2;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 0.00017;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRF 66
              ||||||||||||
Db        147 GNDIAFHFNPRF 158


RESULT 3
A54889
IgE-binding protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54889; A23148
R;Albrandt, K.; Orida, N.K.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6859-6863, 1987
A;Title: An IgE-binding protein with a distinctive repetitive sequence and homology with
A;Reference number: A54889; MUID:88016189; PMID:2958848
A;Accession: A54889
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-262 <ALB>
A;Cross-references: UNIPROT:P08699; GB:J02962; NID:g203173; PIDN:AAA40828.1; PID:g203174
R;Liu, F.T.; Albrandt, K.; Mendel, E.; Kulczycki Jr., A.; Orida, N.K.
Proc. Natl. Acad. Sci. U.S.A. 82, 4100-4104, 1985
A;Title: Identification of an IgE-binding protein by molecular cloning.
A;Reference number: A23148; MUID:85216641; PMID:3858867
A;Accession: A23148
A;Molecule type: mRNA
A;Residues: 125-262 <LIU>
A;Cross-references: GB:M13697; NID:g204727; PIDN:AAA41378.1; PID:g204728
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin; phosphoprotein

  Query Match             3.9%;  Score 12;  DB 2;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.00018;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         55 GNDIAFHFNPRF 66
              ||||||||||||
Db        164 GNDIAFHFNPRF 175


RESULT 4
A46631
lactose-binding lectin L-36 - rat
N;Alternate names: galectin-4
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46631; S69096
R;Oda, Y.; Herrmann, J.; Gitt, M.A.; Turck, C.W.; Burlingame, A.L.; Barondes, S.H.; Leff
J. Biol. Chem. 268, 5929-5939, 1993
A;Title: Soluble lactose-binding lectin from rat intestine with two different carbohydra
A;Reference number: A46631; MUID:93194902; PMID:8449956
A;Accession: A46631
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-324 <ODA>
A;Cross-references: UNIPROT:P38552; GB:M73553; NID:g294571; PIDN:AAA41505.1; PID:g294572
A;Experimental source: intestine
A;Note: sequence extracted from NCBI backbone (NCBIN:128409, NCBIP:128410)
R;Tardy, F.; Deviller, P.; Louisot, P.; Martin, A.
FEBS Lett. 359, 169-172, 1995
A;Title: Purification and characterization of the N-terminal domain of galectin-4 from r
A;Reference number: S69096; MUID:95172227; PMID:7867792
A;Accession: S69096
A;Molecule type: protein
A;Residues: 13-37;44-50,'E',52-66 <TAR>
C;Superfamily: lactose-binding lectin L-36
C;Keywords: lectin

  Query Match             3.2%;  Score 10;  DB 2;  Length 324;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         57 DIAFHFNPRF 66
              ||||||||||
Db         59 DIAFHFNPRF 68


RESULT 5
S08576
lectin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S08576
R;Raz, A.; Carmi, P.; Pazerini, G.
Cancer Res. 48, 645-649, 1988
A;Title: Expression of two different endogenous galactoside-binding lectins sharing sequ
A;Reference number: S07162; MUID:88080093; PMID:3335026
A;Accession: S08576
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <RAZ>
A;Cross-references: UNIPROT:Q61357
C;Superfamily: beta-galactoside-binding lectin

  Query Match             2.6%;  Score 8;  DB 2;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db         72 AFHFNPRF 79


RESULT 6
JC4300
galectin-3 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4300
R;Gaudin, J.C.; Monsigny, M.; Legrand, A.
Gene 163, 249-252, 1995
A;Title: Cloning of the cDNA encoding rabbit galectin-3.
A;Reference number: JC4300; MUID:96011642; PMID:7590275
A;Accession: JC4300
A;Molecule type: mRNA
A;Residues: 1-242 <GAU>
A;Cross-references: UNIPROT:P47845; GB:U06470; NID:g606794; PIDN:AAC48491.1; PID:g606795
A;Experimental source: vascular smooth muscle cells
A;Note: The authors translated the codon TTC for residue 155 as Leu
C;Comment: This protein has the functions on cell adhesion and proliferation. It is a su
C;Genetics:
A;Gene: lgals3
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: muscle

  Query Match             2.6%;  Score 8;  DB 2;  Length 242;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db        148 AFHFNPRF 155


RESULT 7
```

```
A35820
galectin 3 - human
N;Alternate names: CBP 35; epithelial-specific lectin 35; galactoside-binding lectin L-2
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35820; JQ0916; A47473; A36071; A49800
R;Robertson, M.W.; Albrandt, K.; Keller, D.; Liu, F.T.
Biochemistry 29, 8093-8100, 1990
A;Title: Human IgE-binding protein: a soluble lectin exhibiting a highly conserved inter
A;Reference number: A35820; MUID:91084480; PMID:2261464
A;Accession: A35820
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <ROB>
A;Cross-references: UNIPROT:P17931; GB:M57710; NID:g179530; PIDN:AAA35607.1; PID:g179531
R;Oda, Y.; Leffler, H.; Sakakura, Y.; Kasai, K.; Barondes, S.H.
Gene 99, 279-283, 1991
A;Title: Human breast carcinoma cDNA encoding a galactoside-binding lectin homologous to
A;Reference number: JQ0916; MUID:91216471; PMID:2022338
A;Accession: JQ0916
A;Molecule type: mRNA
A;Residues: 1-250 <ODA>
A;Cross-references: GB:M36682; NID:g186921; PIDN:AAA36163.1; PID:g186922
R;Lotz, M.M.; Andrews Jr., C.W.; Korzelius, C.A.; Lee, E.C.; Steele Jr., G.D.; Clarke, A
Proc. Natl. Acad. Sci. U.S.A. 90, 3466-3470, 1993
A;Title: Decreased expression of Mac-2 (carbohydrate binding protein 35) and loss of its
A;Reference number: A47473; MUID:93234518; PMID:7682704
A;Accession: A47473
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-63,'P',65-97,'T',99-250 <LOT>
A;Cross-references: GB:S59012; NID:g299601; PIDN:AAB26229.1; PID:g299602
A;Experimental source: normal colonic mucosa, colon carcinoma, cell line clone A
A;Note: sequence extracted from NCBI backbone (NCBIN:129689, NCBIP:129692)
R;Cherayil, B.J.; Chaitovitz, S.; Wong, C.; Pillai, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 7324-7328, 1990
A;Title: Molecular cloning of a human macrophage lectin specific for galactose.
A;Reference number: A36071; MUID:90384999; PMID:2402511
A;Accession: A36071
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-32,'Q',34,'L',37,'RGFLSWGL',46,'RAGT',51,'R',53-63,'P',65-87,89-250 <CHE>
A;Cross-references: GB:M35368; NID:g1196441
A;Note: the sequence is revised in GenBank entry HUMMAC2, release 113.0, PIDN:AAA88086.1
R;Raz, A.; Carmi, P.; Raz, T.; Hogan, V.; Mohamed, A.; Wolman, S.R.
Cancer Res. 51, 2173-2178, 1991
A;Title: Molecular cloning and chromosomal mapping of a human galactoside-binding protei
A;Reference number: A49800; MUID:91183475; PMID:2009535
A;Accession: A49800
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-32,'Q',34,'LPGASYPGAYPAGTPGLSWTAPPGATMEHVELIRSTCTWSLRTQ',86-104,'A',106,'M
A;Cross-references: GB:M64303; NID:g413862
A;Note: this translation is not annotated in GenBank entry HUMGALBIN, release 113.0
C;Genetics:
A;Gene: GDB:LGALS3; MAC-2; LGALS2
A;Cross-references: GDB:127515; OMIM:137033
A;Map position: 1p13-1p13
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin; nucleus; phosphoprotein

  Query Match              2.6%;  Score 8;  DB 2;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db        156 AFHFNPRF 163


RESULT 8
A28651
galactose-specific lectin - mouse
N;Alternate names: carbohydrate-binding protein 35; IgE-binding protein; lectin L-34; Ma
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1989 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: S08537; A28651; A37385; A35185
R;Cherayil, B.J.; Weiner, S.J.; Pillai, S.
J. Exp. Med. 170, 1959-1972, 1989
A;Title: The Mac-2 antigen is a galactose-specific lectin that binds IgE.
A;Reference number: S08537; MUID:90063462; PMID:2584931
A;Accession: S08537
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-264 <CHE>
A;Cross-references: UNIPROT:P16110; EMBL:X16834; NID:g52986; PIDN:CAA34736.1; PID:g52987
A;Note: this sequence was submitted to the EMBL Data Library, Oct-1989
R;Jia, S.; Wang, J.L.
J. Biol. Chem. 263, 6009-6011, 1988
A;Title: Carbohydrate binding protein 35. Complementary DNA sequence reveals homology wi
A;Reference number: A28651; MUID:88198129; PMID:3360772
A;Accession: A28651
A;Molecule type: mRNA
A;Residues: 'R',3-264 <JIA>
A;Cross-references: EMBL:J03723
R;Raz, A.; Pazerini, G.; Carmi, P.
Cancer Res. 49, 3489-3493, 1989
A;Title: Identification of the metastasis-associated, galactoside-binding lectin as a ch
A;Reference number: A37385; MUID:89275058; PMID:2525069
A;Accession: A37385
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-3,'T',5-91,'ST',94-109,'SAP',113-264 <RAZ>
A;Cross-references: GB:X16074; NID:g52850; PIDN:CAA34206.1; PID:g52851
A;Note: authors translated the codon GAA for residue 219 as Ala, GAC for residue 221 as
R;Woo, H.J.; Shaw, L.M.; Messier, J.M.; Mercurio, A.M.
J. Biol. Chem. 265, 7097-7099, 1990
A;Title: The major non-integrin laminin binding protein of macrophages is identical to c
A;Reference number: A35185; MUID:90236991; PMID:2332426
A;Accession: A35185
A;Molecule type: protein
A;Residues: 159-163;166-175;214-226 <WOO>
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: lectin; phosphoprotein

  Query Match              2.6%;  Score 8;  DB 2;  Length 264;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db        170 AFHFNPRF 177


RESULT 9
A45983
lactose-binding lectin Mac-2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A45983
R;Rosenberg, I.M.; Iyer, R.; Cherayil, B.; Chiodino, C.; Pillai, S.
J. Biol. Chem. 268, 12393-12400, 1993
A;Title: Structure of the murine Mac-2 gene. Splice variants encode proteins lacking fun
A;Reference number: A45983; MUID:93286070; PMID:8509379
A;Accession: A45983
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <ROS>
A;Cross-references: UNIPROT:Q8C253; GB:L08649
C;Genetics:
A;Introns: 6/3; 128/3; 158/2; 209/2; 213/3
C;Superfamily: beta-galactoside-binding lectin

  Query Match              2.6%;  Score 8;  DB 2;  Length 264;
  Best Local Similarity   100.0%;  Pred. No. 3.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         59 AFHFNPRF 66
              ||||||||
Db        170 AFHFNPRF 177


RESULT 10
A49688
lactose-binding lectin L-29 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Nov-1999
C;Accession: A49688
R;Herrmann, J.; Turck, C.W.; Atchison, R.E.; Huflejt, M.E.; Poulter, L.; Gitt, M.A.; Bur
J. Biol. Chem. 268, 26704-26711, 1993
A;Title: Primary structure of the soluble lactose binding lectin L-29 from rat and dog a
agenase.
A;Reference number: A49688; MUID:94075368; PMID:8253805
A;Accession: A49688
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <HER>
A;Cross-references: GB:L23429
C;Superfamily: beta-galactoside-binding lectin
C;Keywords: acetylated amino end
F;1/Modified site: acetylated amino end (Ala) #status experimental

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Qy         59 AFHFNPRF 66
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Db        200 AFHFNPRF 207


RESULT 11
A55975
galectin-8 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A55975
R;Hadari, Y.R.; Paz, K.; Dekel, R.; Mestrovic, T.; Accili, D.; Zick, Y.
J. Biol. Chem. 270, 3447-3453, 1995
A;Title: Galectin-8. A new rat lectin, related to galectin-4.
A;Reference number: A55975; MUID:95155445; PMID:7852431
A;Accession: A55975
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-316 <HAD>
A;Cross-references: UNIPROT:Q62665; GB:U09824; NID:g717031; PIDN:AAA66359.1; PID:g717032
C;Superfamily: lactose-binding lectin L-36

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  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db         62 AFHFNPRF 69


RESULT 12
JC6147
prostate carcinoma tumor antigen 1 - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 29-Sep-1999
C;Accession: JC6147
R;Su, Z.Z.; Lin, J.; Shen, R.; Fisher, P.E.; Goldstein, N.I.; Fisher, P.B.
Proc. Natl. Acad. Sci. U.S.A. 93, 7252-7257, 1996
A;Title: Surface-epitope masking and expression cloning identifies the human prostate ca
A;Reference number: JC6147; MUID:96293510; PMID:8692978
A;Accession: JC6147
A;Molecule type: mRNA
A;Residues: 1-317 <SUA>
A;Cross-references: GB:L78132; NID:g1932711; PIDN:AAB51605.1; PID:g1932712
C;Comment: This protein is a therapeutic reagent for intervention in pervasive and fatal
tein is a member of the gelectin familly.
C;Superfamily: lactose-binding lectin L-36
C;Keywords: tumor

  Query Match             2.6%;  Score 8;  DB 2;  Length 317;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
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Qy         59 AFHFNPRF 66
              ||||||||
Db         63 AFHFNPRF 70


RESULT 13
A55664
lectin L-36 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C;Accession: A55664
R;Chiu, M.L.; Parry, D.A.D.; Feldman, S.R.; Klapper, D.G.; O'Keefe, E.J.
J. Biol. Chem. 269, 31770-31776, 1994
A;Title: An adherens junction protein is a member of the family of lactose-binding lecti
A;Reference number: A55664; MUID:95081129; PMID:7989350
A;Accession: A55664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-323 <CHI>
A;Cross-references: UNIPROT:Q29058; GB:X79303; NID:g623345; PIDN:CAA55884.1; PID:g623346
C;Superfamily: lactose-binding lectin L-36

  Query Match             2.6%;  Score 8;  DB 2;  Length 323;
  Best Local Similarity   100.0%;  Pred. No. 3.8;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 AFHFNPRF 66
              ||||||||
Db         61 AFHFNPRF 68


RESULT 14
AD2580
two component sensor kinase Atu0027 [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2580
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-881 <KUR>
A;Cross-references: UNIPROT:Q8UJA1; GB:AE008688; PIDN:AAL41058.1; PID:g17738345; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0027
A;Map position: circular chromosome

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  Best Local Similarity   100.0%;  Pred. No. 9.7;
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Qy        197 ILLSGTVL 204
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Db         69 ILLSGTVL 76
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RESULT 15
C97362
protein sensor protein (AF042096) [imported] - Agrobacterium tumefaciens (strain C58, Ce
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97362
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97362
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-881 <KUR>
A;Cross-references: UNIPROT:Q8UJA1; GB:AE007869; PIDN:AAK85852.1; PID:g15154889; GSPDB:G
C;Genetics:
A;Gene: AGR_C_44
A;Map position: circular chromosome

Query Match 2.6%; Score 8; DB 2; Length 881;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 ILLSGTVL 204
||||||||
Db 69 ILLSGTVL 76

Search completed: July 13, 2005, 08:02:31
Job time : 42 secs